Run on:

9, 2003, 08:08:56 ; Search time 29.7313 Seconds (without alignments) 268.471 Million cell updates/sec

83

Title: Perfect score:

US-09-928-048A-4 422 1 VSEIQLMHNLGKHLNSMERV......KSLGEANKADVNVLTKAKSQ Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	parathyroid hormon							æ	Leucine-tRNA 110as	- 5-		chromosome assembl				~	hypothetical prote	DNA-damage repair	probable chromosom	prophage p13 prote	chromosome-asserta	GMP kinase [import	- 24	hypothetical prote		probable flagellar			succinoglycan bios
SOMMAKIES		OI.	PTHU	JC4202	PTBO	PTPG	A05091	151851	A34937	G89813	F72408	I58383	T44010 .	B70356	E82046	C71438	B71438	F56653	T23195	G96934	F84669	нв6803	T23744	A86506	F72117	T40253	T43497	D81401	E70207	A71407	A96232
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		Length DB	115	115	115	115	115	105	119	565	824	1257	555	1156	443	655	674	378	215	396	1163	283	1244	205	202	1018	166	642	417	487	797
de	Query	Match	98.8	86.7	85.1	84.1	73.7	71.8	41.4	17.3	17.2	17.1	16.5	•	15.9	•	15.9	15.8	15.6	15.6	15.6	15.4	15.4	15.3	15.3	15.3	15.2	15.2	15.0	15.0	15.0
		Score	417	366	359	355	311	303	174.5	73	72.5	. 72	69.5	67.5	67	67	φ	66.5	99	. 99	99	65	65	64.5	. 64.5	64.5	64	64	63.5	ب	63.5
	Result	No.	1	7	m	4	·	9	7	a	on ;	10	11	12	13	14	15	16	17	18	19	50	21	22	23	. 24	25	56	27	28	29

hypothetical prote	adaptor protein in	probable methyltra	total bearage	roof protein home	protein-tyrogine k	Fit3 protein - mon	MG328 homolog P01	myosin heavy chain	transcription fact	hypothetical prote	ج.	hypothetical prote	hypothetical prote	low affinity nento	low affinity penic
AD3054	T09194	T37558	T42186	A05028	A39931	S18827	873693	138055	I38414	F82884	D64650	T34156	T29291	S54182	S54178
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797	1270	108	672	862	992	1000	1033	1937	2109	5005	370	415	209	673	674
15.0	15.0	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.8	14.8	14:8	14.8	14.8
63.5	63.5	. 63	63	63	63	63	63	63	63	63	62.5	62.5	62.5	62.5	62.5
30	31	35	33	34	35	36	37	38	36	40	41	42	43	44	45
														•	

ALIGNMENTS

7	
SULT	DH.

RESULT 1
PATHU

Parathyroid hormone precursor (validated) - human
N.Alternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
C;Accession: Al9339; S53790; A931789; A93789; A93783; A90887; A90426; A94
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Pott
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-213i, 1983
A;Title: Nucleotide sequence of the human parathyroid hormone gene.
A;Atference number: Al9339; MUID:83169834; PMID:6220408

A; Molecule type: DNA A; Residues: 1-115 <VAS. A; Residues: 1-115 <VAS. A; Cransparences: GB:J00301; NID:g190702; PIDN:AAA60215.1; PID:g190704 B; Yamaguchl, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K. Biol. Chem. Hoppe-Seyler 375, 821-824, 1994 A; Title: Purification of meprin from human kidney and its role in parathyroid ho. A; Reference number: S53790; MUID:95225988; PMID:7710697

A; Molecule type: protein
A; Residues: 'X', 33, 'X', 35, 46; 65-84; 105-110 < YAM>
A; Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also
R; Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974.

A;Title: Structural analysis of human proparathyroid hormone by a new microseque A;Reference number: A93169; MUID:74174967; PMID:4833516 A;Accession: A93169

A;Molecule type: protein A;Mesidues: 26-37 <AAC. R;Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gaut: Eur. J. Blochem. 205, 311-319, 1992

A.Title: Isolation and characterization of two biologically active O-glycosylate.

A) Reference number: S21199; MUID:92209518; PMID:1555591 A; Accession: S21199

A Molecule type: protein
A; Mesiduces: 32-114,/N' www.ncbs//www.

A; Accession: A93789

A; Molecule type: protein A; Residues: 32-68 <NIA>

R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D. Proc. Natl. Acad. Sci. U.S.A. 69, 3865-3858, 1972.
A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal res. A;Reference number: A93783; MUID:73070429; PMID:4509319

A; Accession: A93783 A; Molecule type: protein

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C; Accession: JC4202
R; Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Cagene 160, 241-243, 1995
A; Title: Sequences of the CDNAs encoding canine parathyroid hormone-related pray; A; Accession: JC4201; MUID:95369696; PMID:7642102
                                                                                                                                                                           Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:U15662; NID:9558915; PIDN:AAA82584.1; PID:9558916 C;Superfamily: parathyroid hormone; parathyroid hormone homology C;Keywords: hormone
                                                                                                            ne precursor - dog
lupus familiaris (dog)
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A; Residues: 26-115 <HAM>
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A; Residues: 1-115 <ROS>
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A; Residues: 75-100 (KEZ>
A; Residues: 75-100 (KEZ>
A; Residues: 75-100 (KEZ>
B; Tregear, G.W; van Rileschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J. Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A; Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum A; Reference number: Ajlofo; MUTD:75059220; PMID:4444131
A; Reference number: Ajlofo; MUTD:75059220; PMID:4444131
A; Note: the biologically active amino-terminal 34 residues of parathyroid hormone were s at renal adenylate cyclase assay and with the bovine hormone's active region in the chic R; Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel, Helv. Chim. Acta 56, 470-473, 1973
A; Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A; Reference number: Ajlof35; MCID:73227467; PMID:472148
A; Contents: annotation; synthesis of residues 32-65
A; Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
                                  mass spectroscopic identification of., Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.M.; Hendy, G.N.; O'Riordan, J.L.
M., and Parsons, J.A., eds., pp.9-
                                                                                                                      A.Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone. A:Reference number: A90387; MUID:75146516; PMID:1125201
A:Accession: A90387
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                                                                                                                                                                                                                                                                                                            Jr., J.T.
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                                                                                                                                                                                                                               A;Molecule type: protein
A;Reaidues: 52-75 <RE3>
R;Keutmann, H. T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts,
Blochemistry 17, 5723-5729, 1978
A;Ttle: Complete amino acid sequence of human parathyroid hormone.
A;Reference number: A90426; MUID:79082855; PMID:728431
A;Accession: A90426
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Pred, No. 5.4e-37;
1; Mismatches 0; Indels
                                                                  .; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: the first intron occurs before the initiator codon
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co. Natl. Acad. Sci. US.A. 78, 7365-7369, 1981
Title: Nucleotide sequence of cloned cDNAs encoding hu
Reference number: 138342; MUID:82150870; PMID:6950381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 61-106, 'D',108-115 <KEU>
R;Reutmann, H.T.; Ntall, H.D.; Jacobs, J.W.; Barling,
in Calcium-regulating Hormones, Talmadge, R.V., Owen,
A;Reference number: A94410
                                      sequenator
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1; Mismatches
32-52, 'Q', 54-58, 'K', 60, 'L', 62-65
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98.88;
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                                                                                                        iochemistry 14, 1842-1847,
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Residues: 1-115 <RES>
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Matches 82;
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parathyroid hormone precursor - bovine (5/5pecies: Bos primigenius taurus (cattle) (c/5pecies: Bos primigenius taurus (cattle) (c/5pecies: 23-0ct-1981 #sequence_revision 23-0ct-1981 #text_change 18-Jun-1999 (c/5dccession: A24949; A33793; A91648; A93773; I45975; I45976; A01534 R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B. A/fitle: Isolation and complete nucleotide sequence of the gene for bovine para A/Feference number: A24949; MuID:84262483; PMID:6086460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1.115 (WEA>
(Cross-references: GB:K01938
Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Pc.
roc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979
Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathy
Reference number: A93835; MuiD:80056617; PMID:388425
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-115 < RON
A; Cross references: GB: V00106; GB: J000023; NID: 984; PIDN: CAA23439.1; PID: 985
A; Cross references: GB: V00106; GB: J00003; NID: 984; PIDN: CAA23439.1; PID: 985
A; Note: the authors translated the codon GAA for residue 50 as Gly
A; Note: the authors translated the codon GAA for residue 50 as Gly
B; Hamilton, J W.; Nall, H.D.; Jocoba, J W.; Keutmann, H.T.; Potts Jr., J.T.;
Broc. Natl. Acad. Sci. U.S.A. 71, 633-656, 197
A; Title: The N terminal anino-acid sequence of bovine proparathyroid hormone.
A; Reference number: A93793; MUID: 74142666; PMID: 4522780
                                                                                                                                                                                                                                                                                                                                           1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                            ..
                                                                                                                                                                        Length 115;
F:1-31/Domain: signal sequence #status predicted <SIG>F:30-64/Domain: parathyroid hormone homology <PTH>F:32-115/Product: parathyroid hormone #status predicted <MAT>
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                   Query Match 86.7%; Score 366; DB 2; L
Best Local Similarity 86.7%; Pred. No. 1.3e-31;
Matches 72; Conservative 6; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A.
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m

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A; Molecule type: protein
A; Mesidues: 32-109 '<3AD.
R; Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A; Title: Recent studies on the chemistry of human, bovine and porcine perathyroid
A; Reference number: A90030; MUID:74173303; PMID:4598526
                                                                                                                    biosynthesis, and parti
                                                                                                                                                                                                                                                                                                   Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Pott: 1974
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C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
C:Accession: A05091; A2580
F:Heinrich, G:/ Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A:Reference number: A05091; MUID:84135846; PMID:6321505
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    L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Jemistry 14, 3631-3635, 1975

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: parathyroid hormone; parathyroid hormone homology C; Keywords: calcium; hormone; parathyroid gland F;1-25/Domain: signal sequence fstatus predicted <SIG>F;26-31/Domain: propeptide fstatus experimental <PRO>F;30-64/Domain: parathyroid hormone homology <PRH>F;32-115/Product: parathyroid hormone fstatus experimental <MAT>
                                                                                                                                                                                                                 A Molecule type: protein
A; Residues: 26-115 <CHU>
B; Sauer, R.T.; Miall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riord
B! Ochemistry 13, 1994-1999, 1974
A; Title: The amino eaid sequence of porcine parathyroid hormone.
A; Reference number: A90376; MUID: 74253317; PMID: 4840833
A; Accession: A90376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 355; DB 1; Length 115;
Pred. No. 1.9e-30;
6; Mismatches 7; Indels
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C; Superfamily: parathyroid hormone; parathyroid hormone homology
F; 30-64/Domain: parathyroid hormone homology <PTH>
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A;Residues: 1-115 <HEI>
A;Cross-references: GB:K01268; NID:g206483; PIDN:AAA41979.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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A;Reference number: A26806; MUID:87316938; PMID:3628009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 73.7%; Score 311; DB 2; I Best Local Similarity 72.3%; Pred. No. 8.4e-26; Matches 60; Conservative 11; Mismatches 12;
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84.3%; Pred. No. 1.5
6; Mismatches
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A; Residues: 1-115 <SCH>
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Matches
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                                                                                                     A.Molecule type: protein
A.Residues: 32-115 cBRE>
A.Residues: 32-115 cBRE>
R.Potts Jr., Jr.; Tregerar, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.;
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
A.Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyr
A.Reference number: A3776; Mullo;1001588; PMID:432265
A.Note: the synthetic peptide was active in vivo and in vitro
A.Note: the synthetic peptide was active in vivo and in vitro
A.Note: the synthetic peptide was active in vivo and in vitro
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R.Wawarr, C.A.; Gordon, D.F.
R.Wawarr, C.A.; Gordon, D.F.
A.Title: Introduction by molecular cloning of artifactual inverted sequences at the 5'
A.Reference number: 145975; WUID:82037785; PMID:6170060
A.Reference number: 144975
A.Reference number: Idensiated from GB/EMBL/DDBJ
A.Recession: Idensiaty: translated from GB/EMBL/DDBJ
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C;Accession: B26606; A90376; A01535
R;Schmelzer, H.J; Gross, G; Widera, G; Mayer, H.
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A:Molecule type: mRNA
A:Molecule type: mll 444, 1982
A:Molecule type: mll 444, 1982
A:Molecule type: mll 45976; MulD:83105964; PMID:6185374
A:Accession: 145976
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Genetics:
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F.26-115/Product: proparathyroid hormone #status experimental <PMAT>
F.26-31/Domain: propeptide #status experimental <PRO>
F.30-64/Domain: parathyroid hormone homology <PTH>
F:30-64/Domain: parathyroid hormone #status experimental <MAT>
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C; Keywords: hormone
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llarity 85.5%; Pred. No: 7.2e-31;
Conservative 5; Mismatches 7; Indels
A;Title: Bovine parathyroid hormone: amino acid sequence.
A;Reference number: A93773; NUID:71063634; PMID:5275384
A;Accession: A93773
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A;Residues: 1-115 <SCH>
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Matches 71;
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C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Datession: 689813
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimi C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1255-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Cross-references: GB:AE001702; GB:AE000512; NID:g4980662; PIDN:AAD35261.1; PIC
                                                                                                                                                                                                                                                                                        DNA polymerase III gamma and tau subunits [imported] - Staphylococcus aureus (si
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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richar
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Ajitle: Evidence for lateral gene transfer between Archaea and Bacteria from g
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:BA000018; PID:g13700368; PIDN:BAB41666.1; GSPDB:GN00149
A;Experimental source: strain N315
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. 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE
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C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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                                                                                                                                    81
                                                 33 VSEMOLMHNLGEHRHTVERODWLOMKLODVHS----
                                                                                                     --SHEKSLGEANKADVNVLTKAK
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23.3%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73;
Pred. No. 7
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Matches 20; Conservative
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nes 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-565 <KUR>
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A; Gene: dnaX
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Matches
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11. Endocrinol. 3, 325-331, 1989
11. Endocrinol. 3, 325-331, 1989
11. Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyromaterence number: A34937; MUID:89219100; PMID:2710135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:M31604; NID:g212767; PIDN:AAA49093.1; PID:g212768
Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.
Bone Miner. Res. 3, 689-698, 1988
Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.
Reference number: 150411; MUID:89284968; PMID:3251402
Accession: 150411
                                                                                                                                                                                                                                                                                                                                                                iv. Gene Technol. 21, 228-229, 1984
Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
Reference number: 151851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 VSEIQLMHNLGKHLASVERMQWLRKKLQDVHNFVSLGVQMAAREGSYQRPTKKEENVLVD 92
                                                                                                                                                                                                                 parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 151851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          es: Gallus gailus (chicken)
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Superfamily: parathyroid hormone; parathyroid hormone homology.
1-25/Domain: signal sequence *status predicted <SIG>-26-31/Domain: propeptide *status predicted <PRO>30-64/Domain: parathyroid hormone homology <PTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: M54875; NID: g601932; PIDN: AAA57156.1; PID: g601933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: parathyroid hormone; parathyroid hormone homology 20-54/Domain: parathyroid hormone homology <Pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.8%; Score 303; DB 2;
69.9%; Pred. No. 5.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
Residues; 1-105 <RES>
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12; Mismatches
                                                                             GNSKSLGEGDKADVDVLVKAKSQ 115
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                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - chicken
                                                    SHEKSLGEANKADVNVLTKAKSQ
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nes 58; Conservative
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Best Local Similarity
Matches 42; Conserv
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Residues: 1-119 <RUS>
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A,Title: Comparison of the complete DNA sequences of human herpesvirus 6 variant A;Reference number: 222732; MUID:99412319; PMID:10482554 A;Accession: T44010 A;Accession: T44010 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Human herpesvirus 6B genome sequence: coding content and comparison wit. A; Reference number: 222734; MUID:99412318; PMID:10482553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross references: EMBL:AB021506; NID:g4995977; PIDN:BAA78271.1; PID:g4996038; Experimental source: strain HST; pop. variant B. Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, Virol. 73, 8040-8052, 1999
                                                                                                                                                                                                                                                                                                                                            C; Accession: T44010; T44197
R: Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa,
J. Virol. 73, 8053-8063, 1999
                                                                                                                                                                                                                                                                              C:Species: human herpesvirus 6
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                       - human herpesvirus 6
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1 Similarity 35.4%;
23: Conservative 10
                                                                 1236 SDTGMSPSSSS 1246
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                             ADVNVLTKAKS
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A; Residues: 1-555 <ISE>
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;Cross-references: GB:S66427; NID:9435775; PIDN:AAB28543.1; PID:9435776
;Otterson, G.A.; Kratzke, R.A.; Lin, A.Y.; Johnston, P.G.; Kaye, F.J.
;ncopene 8, 949-957, 1993
;Title: Alternative splicing of the RBP1 gene clusters in an internal exon that encodes
;Reference number: IS8390; MUID:93205410; PMID:8455946
                                                                                                                                                                                                                                                                                                                                                                          Species: Homo sapiens (man)
Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
Pactages 17-Mar-2000 #sequence_revision 17-Mar-2000
Pactages 8, 3149-3156, 1993
Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
Reference number: 158383; MUID:94020841; PMID:8414517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNA

Mesdidues: 338-384, V, V, 386-617, R, 618-652, VV, 654-778, T, 780-1120,1175-1257 < OTT2>

Gross-references: GB:S57160; NID:9298683; PIDN:AAB25834.1; PID:9298684

Defec-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuccolo, G.A.; Hanobik, M.G.

Title: Cloning of CDNAs for cellular proteins that bind to the retinoblastoma gene pro-

Reference number: S16953; MUID:91312450; PMID:1857421
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;Molecule type: mrnA
;Residues: 855-1177, 8',1179-1195, SENIICL' <DEF>
;Residues: 855-1177, 8',1179-1195, SENIICL' <DEF>
;Raelin Jr., W.G.; Krek, W.; Sellers, W.R.; Decaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.
ell 70, 351-364, 1992
filtle: Expression cloning of a CDNA encoding a retinoblastoma-binding protein with E2F
;Reference number: A42997; MuID:92346721; PMID:1638635
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C;Superfamily: human retinoblastoma binding protein 1
C;Reywords: alternative splicing
F;1-1257/Product: retinoblastoma binding protein 1, splice form I #status predicted <SF1
F;1-1120,1175-1257/Product: retinoblastoma binding protein 1, splice form II *status pre
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Note: the cited GenBank accession number, M96577, is apparently a misprint and does
Note: sequence extracted from NCBI backbone (NCBIN:110020, NCBIP:110022)
592 MELVNHLSOYLNSVPQEEWNRKLLREIVEKLTLALSPFAPHLAEEFWHDLGN-----D 744
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Residues: 338-384,'V',386-617,'R',619-652,'V',654-778,'T',780-1257 <OT
Cross-references: GB:S57153; NID:9298681; PIDN:AAB25833.1; PID:9298682
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N.Alternate names: retinoblastoma-associated protein 2 (misno
N.Contains: retinoblastoma binding protein 1, splice form II
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Residues: 'MMTMKL',510-617,'R',619-1257 <KAE>
                                                                                                         SLVVQQSWPSYDPKALEVEEVEIAIQINGK
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A;Cross-references: GDB:120340; OMIM:180260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 19; Conserv
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: L1156 CAQF> A;Essidues: 1-1156 CAQF> A;Cross-references: GB:AE000699; NID:92983238; PIDN:AAC06839.1; PID:92983243; GB:C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Aquifex aeolicus
Date: 08-May-1998 #sequence_revision 08-May-1998 *text_change 02-Jun-2000
Accession: B70356
                                                                                                                                                                                                                                                                                                                             23 LRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEA----NKADVNVLT
                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                        Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1156;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome assembly protein homolog - Aquifex aeolicus
                                                                                                                                                                          C: Superfamily: varicella-zoster virus gene 34 protein
                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-555 <DOM>
                                                                             A;Cross-references: EMBL:AF157706; PIDN:AAB06348.1
A;Experimental source: strain 229; variant B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: xcpC
C;Superfamily: chromosome segregation protein SMC1
                                                                                                                                                                                                                                  ; Score 69.5; D
; Pred. No. 16;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 29.0%; Pred. No. 61;
Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.0%; Score 67.5; 29.0%; Pred. No. 61
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Best Local
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Gaps

25;

Indels

25;

13 HLNSMERVEWLRKKLØDVHN-FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANK

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CiAccession: B71438
R; Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, P.; Wedler, H.; Wedler, E.; Wanbutt, R.; Weitzeneger, T.; Pohl, T.M.; Terryn, avanagh, T.; Hempel, S.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; F. Nature 391, 485-488, 1998
Nature 391, 485-488, 1998
Ashathors; Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pul erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman C.; Chalwatzis, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabido A;Reference number: A71400; MUD:98121113; PMID:9461215 A;Accession: B71438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
                                    12 KHINSMER-VEWLRKKLODVHNFVALGAPLAPRDAGSORPRKK---EDNVLVESHEKSLG 67
12 KHLNSMER-VEWLRKKLODVHNFVALGAPLAPRDAGSORPRKK---EDNVLVESHEKSLG 67
                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Arabidopsis thaliana (Sciense) C.Species: Arabidopsis thaliana (mouse-ear cress) Arabidopsis thaliana (mouse-ear cress) A.Variety; columbia A.Variety; columbia C.Date: 03-Aug-1998 *sequence_revision 03-Aug-1998 *text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 15.9%; Score 67; DB 2; Length 674; Best Local Similarity 24.3%; Pred. No. 38; Matches 18; Conservative 21; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-674 <BEV>
A;Residues: 1-674 <BEV>
A;Cross-references: GB:Z97342; NID:g2245031; PID:g2245057
C;Genetics:
A;Map position: 4COP9-4G3845
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                                                                                                                                                                   : :||::|
312 DTSKANMNNQLQAR 325
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                                                                                                                              EANKADVNVLTKAK 81
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Job time: 32.7313 secs
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                                                                                                                                                                                                                                                                                                                                              proteinase Hslvu, ATPase subunit Hslu VC2674 [imported] - Vibrio cholerae (strain N16961
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 *sequence_revision 20-Aug-2000 *text_change 02-Feb-2001
C:Accession: E82046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Regidues: 1-443 <HEL>
A; Regidues: 1-443 <HEL>
A; Cross-references: GB: AE004333; GB: AE003852; NID: 99657266; PIDN: AAF95815.1; GSPDB: GN001
A; Experimental source: serogroup 01; strain N16961; blotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis that A; Reference number: A71400; MUID:98121113; PMID:9461215
A; Accession: C71438
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C;Superfamily: heat shock protein hslU; FtsH/SEC18/CDC48-type ATP-binding domain homolog
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erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Heddelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
A.R. 477-483, 2000
A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A.Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Arabidopsis thallana
C:Species: Arabidopsis thallana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C;Accession: C71438
R;Bevan, M; Bancroft, I; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Punk, I; Hempel, S.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, Nature 391, 485-488, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA Residues: 1-655 <BEV>
   ---VEWLRKKLQDVHNFVALGAPLAPRDAGSQRPR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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15.9%; Score 67; DB 2; Length 655;
Best Local Similarity 24.3%; Pred. No. 36;
Matches 18; Conservative 21; Mismatches 31; Indels
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                                    |||||: | | ||:||
794 VSEIE-----KSLNEIERELNKKTYELEYLEKEIQEKER--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.9%; Score 67; DB 2; 28.8%; Pred. No. 23; Live 16; Mismatches 2;
                                                                                                                                                                                       839 LKKEIENLILFKEKTLQEVKEAEVKVYDYIKOK 871
                                                                                                                           52 -KKEDNYLVESHEKSLGEANKADVNYLTKAKSQ 83
   VSEIQLMHNLGKHLNSMER---
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Best Local Similarity 28.8%
Matches 19; Conservative
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Gaps

Parathyroid hormon Human parathyroxin Human parathyroid Human parathyroid Human PTH peptide

parathyroid

Salmon calcifoning Parathyroid hormon Human parathyroid Human bloactive parathyroid Sequence of human Sequence of human Ruman prepro-PTH.

Oxidation resistan Oxidation resistan Coxidation resistan Ruman Parathyroid Human parathyroid

Human PtH(1-84) pe Oxidation resistan Oxidation resistan Oxidation resistan Stability-enhanced Sequence of varian Sequence of varian Sequence of varian Oxidation resistan Stability-enhanced Sequence of varian Oxidation resistan Stability-enhanced Sequence of varian Nation resistan Stability-enhanced Sequence of varian

OM protein

Run on:

Database

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID . Description	ABG74230	AAB07464 Amino acid secuence	•						
	90	24	21	24	21	24		13	14	
	Query Match Length DB	83	84	84	83	83	84	84	84	4
ď	Ouery	100.0	100.0	100.0	99.1	1.66	98.8	98.8	98.8	8
	Score	422	422	422	418	418	417	417	417	417
	Result No.	н	71	m	4	ın	9	7	œ	

Human parathyroid hormone-based CIP, PTH2-84

Parathyroid hormone; PTH; cyclase activating parathyroid hormone; CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium; PTH2-84.

Homo sapiens

US2002160945-A1. 31-OCT-2002. 10-AUG-2001; 2001US-0928047

10-AUG-2000; 2000US-22446P

(CANT/) CANTOR T L.

Cantor TL;

PI; 2003-209227/20

Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises

84 AA;

Sequence

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The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone peptide (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PPH, Which regulates extracellular calcium levels) antagonist activity or reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PPH2-84, PPH3-84 and PPH3-84 (appearing as ABG74230-ABG74233). The present sequence is the CIP PTH2-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragments of PTH function as PTH antagonists. The specification the specification of PTH function as PTH antagonists. The specification substantially normal parathyroid function and having hyperparathyroidism. The method comprises determining and comparing at least two of the following parameters: whole parathyroid hormone level, parathyroid hormone inhibitory peptide fragment level and total parathyroid hormone level. The method is used for monitoring (treatments of) parathyroid related bone disease and the effects of therapeutic treatment for
                                                                                                                                                                                                                                                                                                                                                    VSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperparathyroidism comprises determining and comparing whole parathyroid hormone, parathyroid hormone inhibitory peptide fragment and/or total parathyroid hormone levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
administering a cyclase inhibiting parathyroid hormone peptide
                                                                                                                                                                                                                                                               100.0%; Score 422; DB 24; Length 83; 100.0%; Pred. No. 5.6e-42; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid sequence of human parathyroid hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                        SHEKSLGEANKADVNVLTKAKSO
                                                                                                                                                                                                                                                                                                                                                                                                      SHEKSLGEANKADVNVLTKAKSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Differentiating between normal
                                    Page 3; 8pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCAN-) SCANTIBODIES LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JAN-1999; 99US-0231422.
26-JUN-1999; 99US-0344639.
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                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-0CT-2000
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                                                                                                                                                                                                                                                                                                 83;
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                                                                                                                                                                                                                              Sequence
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                                                               The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone peptide (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PPH, which regulates extracellular calcium levels) antagonist activity to reduce the occurrence of hypercalcaemia or osteosarcome in the patient resulting from the administration of CAP. The peptide comprises PTH2-84, PTH3-84, PTH3-84 and PTH28-84 (appearing as ABG74230 upon which the CIP peptides are based:
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                                                 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNPVALGAPLAPRDAGSQRPRKKEDNVLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                            Parathyrold hormone; PTH: cyclase activating parathyrold hormone; CAP; cyclase inhibiting parathyrold hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide
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  Length
                            Indels
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 Score 422; DB 21;
Pred. No. 5.7e-42;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 422; DB 24;
Pred. No. 5.7e-42;
Mismatches 0;
                                                                                                                                                                                                                                                                     Human full length parathyroid hormone.
                                                                                                   61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                              84
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                                                                                                                                                                                             Ā
                                                                                                                  61 SHEKSLGEANKADVNVLTKAKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 1; 8pp; English.
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                                                                                                                                                                                          ABG74234 standard; peptide; 84
100.08;
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            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-209227/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CANT/) CANTOR T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 AA;
                                                                                                                                                                                                                                                                                                                                                                         US2002160945-A1.
                                                                                                                                                                                                                                                                                                                                                  Homo. saptens.
                                                                                                                                                                                                                                             16-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cantor TL;
                                                                                                                                                                                                                    ABG74234;
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Best Local S
Matches 83
Query Match
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91JP-0056434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
          Parathyroid hormone;
                                                                                                                                                                                                                                WPI; 2003-209227/20
                                                                                                                                                                                (CANT/) CANTOR T L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
tes 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               82 AA;
                                                                              JS2002160945-A1
                                                          Homo saplens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
20-MAR-1991;
                                                                                                                                                                                                         Cantor TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR23790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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AAR23790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a fragment of human parathyroid hormone (PTH), comprising residues 3-84, which functions as a PTH antagonist. The specification describes a method for differentiating between a person having substantially normal parathyroid function and having hyperparathyroidism. The method comprises determining and comparing at least two of the following parameters: whole parathyroid hormone level, parathyroid hormone inhibitory peptide fragment level and total parathyroid hormone level. The method is used for monitoring (treatments of) parathyroid related bone disease and the effects of
                                                                                                                                                                                                                                                                                                                                                                      Differentiating between normal parathyroid function and hyperparathyroidism comprises determining and comparing whole parathyroid hormone, parathyroid hormone inhibitory peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                          Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
                                                                                                                                     of human parathyroid hormone antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 418; DB 21; Length 82;
Pred. No. 1.6e-41;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapeutic treatment for hyperparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human parathyroid hormone-based CIP, PTH34-84,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.1%; Scor.
100.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                               and/or total parathyroid hormone levels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 42-43; 46pp; English,
SHEKSLGEANKADVNVLTKAKSQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 HEKSLGEANKADVNVLTKAKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG74231 standard; peptide; 82
                                                                                                                                                                                                                                                                                                                        (SCAN-) SCANTIBODIES LAB INC.
                                                        AAB07465 standard; protein;
                                                                                                                                                                                                                                                           13-JAN-2000; 2000WO-US00855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; Conservative
                                                                                                                                     Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-476147/41.
                                                                                                                                                                                                            WO200042437-A1.
                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                    14-JAN-1999;
26-JUN-1999;
                                                                                                            20-OCT-2000
                                                                                                                                                                                                                                   20-JUL-2000
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                                                                                   AAB07465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone peptide (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PTH, which regulates extracellular calcium levels) antagonist activity to reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PTH2-84, PTH34-84 and PTH28-84 (appearing as ABG74230-ABG74233). The present sequence is the CIP PTH34-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parathyroid hormone;
CIP; ostennost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide .
                                            CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium; PTH34-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.1%; Score 418; DB 24;
100.0%; Pred. No. 1.6e-41;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hPTH; hypoparathyroidism; osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HEKSLGEANKADVNVLTKAKSO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEKSLGEANKADVNVLTKAKSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 3; 8pp; English.
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1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PTH refers to the mature form of the hormone, which consists of 84 amino acids arranged in the sequence reported by Kimura et al, 1983, Brochem. Blophys. Res. Comm., 114(2):493.
Examples of variants are given in AAR2845.48 and AAR29561-69.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                Variants of PTH exhibiting PTH activity and reduced sensitivity to oxidation are obtained by replacing at least one Met residue in PTH approximation are obtained by replacing at least one Met residue is ofther than Met and Cys.

The Met amino acids are indicated in the Features Table.

The variant may be obtd. using recombinant technique, and may be used for treating osteoporosis, other bone-related disorders.

PSOSIBSIS and cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteolytic;
                                   New oxidn. resistant variants of parathyrold hormone - used for treating osteoporosis, psoriasis and cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                              Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25..27
/note= "ArgLysLys which may be mutated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resistance;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 417; DB 13;
Pred. No. 2.2e-41;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTH; hPTH; stability-enhanced; mutant; resista
enzymes; osteoporosis; bone-related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLY ) ALLELIX BIOPHARMACEUTICALS INC. GLAX ) GLAXO CANADA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHEKSLGEADKADVNVLTKAKSO 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR42067 standard; Protein; 84 AA.
                                                                                    Disclosure, Fig 1; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTH; hPTH; stability-enhanced;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.8%;
Matches 82; Conservative
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human parathyroid hormone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bozzato RP, Kronis KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-336911/42
N-PSDB; AAQ49955.
                                                                                                                                                                                                                                                                                                                                                                            84 AA;
     N-PSDB; AA026498
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05-MAY-1994
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VSEIQLMHNIGKHLINSMERKVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61
                                                                                                                                                                                                              The human parathyroid hormone (hPTH) sequence given is the product of a synthetic gene which corresponds to the amino acid sequence of hPTH. The DNA sequence was produced by enzymatically ligating coligodeoxynucleotides. hPTH is an important regulator of calcium metabolism and has clinical applicns, to diseases such as hypoparathyroidism and osteoporosis. This hPTH can be used as a therapeutic agent or to study the biological role of hPTH in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                               Synthetic gene encoding human parathyroid hormone - formed by ligating oligo-nucleotide(s) and expressed at high yield in E
                                                                                                                                                                                                                                                                                                                                                                                     Score 417; DB 13; Length 84;
Pred. No. 2.2e-41;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parathyroid; hormone; osteoporosis; psoriasis; oxidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALLX ) ALLELIX BIOPHARMACEUTICALS INC. (GLAX ) GLAXO CANADA INC.
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                                                                                                                                                                                   Disclosure; Page 21; 33pp; English.
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                             Fukuda wir masoshika wir sanada yir
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                                                                                                                                                                                                                                                                                                                                                                                   (98.58%)
illarity 98.8%;
Conservative
(TAKE ) TAKEDA CHEM IND LTD.
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91US-0806271
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PTH encoded by px.
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N-PSDB; AAQ24478.
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                                                                                                                                                                                                                                                                                                                                                     84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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13-JAN-1993
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13-DEC-1991;
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RESULT 7

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61

Gaps

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Gaps

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Indels

Length 84;

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1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                            2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VSEIQLMHNIGKHLNSMERVEWLRKKIQDVHNFVALGAPRDAGSQRPRKKEDNVLVE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new method for the isolation and/or purification of a recombinant peptide employs a fusion protein construct (FPC) comprising a carbonic anhydrase and a variable fused polypeptide containing a a fragment of the FPC including the carbonic anhydrase. An alternative method of producing the peptide comprises expressing the FPC as part of a inclusion body. The target peptides of the FPC are pertained from growth hormone releasing factor (GRF), glucagon-like peptide I (GLPI) or parathyroid hormone (FTH). This sequence corresponds to amino acids 1-84 of FTH.
                                                                                                                                                                                                                                                                                                                                                               Parget peptide (PTH(1-84)) used in fusion protein construct
                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein construct; isolation; purification; growth hormone releasing factor; glucagon-like peptide 1; parathyrold hormone; inclusion body; carbonic anhydrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolation and purificn of peptide(s) from fusion protein which include a carbonic anhydrase and a variable fused
                       Score 417; DB 17; Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 417; DB 17;
Pred. No. 2.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holmquist B,
FW;
                                                                  Pred. No. 2.2e
1; Mismatches
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                                                                                                                                                                 ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 58; Page 49; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De LA MOTTE RS, Henriksen DB,
Partridge BE, Stout JS, Wagner
                                                    98.88;
98.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.8%;
                                                                                                                                                                                                                                                                     AAR98954 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-US15800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0350530.
                                                                  Best Local Similarity 98.8
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BION-) BIONEBRASKA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-287186/29.
                       84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De LA MOTTE RS,
                                                                                                                                                                                                                                                                                                                                15-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9617942-A1
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                     Sequence
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                                                  Query Match
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human parathyroid hormone which is used in a new therapeutic preparation for the treatment of osteoporosis. The active substance is in the form of a dry powder suitable for inhalation, in which at least 50% of the dry powder consists of particles of up to 10 microns in diameter or agglomerates of such particles. Pulmonary administration of the parathyroid hormone is effective in the
                                                                                                                                                                                                                                                                              1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for administration by inhalation to treat osteoporosis and stimulate bone formation - comprises parathyroid hormone in form of dry powder mainly of particle size below 10 microns
                                                                                   and sequence is that of human parathyroid hormone (hPTH) which may be mutated in the region Arg25Lys26Lys27 to provide variants with enhanced stability in the presence of proteolytic enzymes such as trypsin.
New parathyroid hormone variants - having aminoacid replacements at positions 25 to 27 to enhance resistance to proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parathyroid hormone; PTH; osteoporosis; inhalation; pulmonary; bone formation.
                                                                                                                                                                                                                       Score 417; DB 14; Length 84;
Pred. No. 2.2e-41;
1; Mismatches 0; Indels
                                                                                                                                                PN field.)
PA field.)
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                                                                                                                                                                                                                                                                                                                                         61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                                                                                                                                                          62 SHEKSLGEADKADVNVLTKAKSQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Pages 15-16; 25pp; English.
                                                                                                                                                (Updated on 25-MAR-2003 to correct (Updated on 25-MAR-2003 to correct
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                                                          Disclosure; Fig 2; 44pp; English.
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                                                                                                                                                                                                                       98.88;
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(first entry)
                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 98.8
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human parathyroid hormone
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                                                                                                                                                                                           84 AA;
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22-DEC-1994;
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24-FEB-1998
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FFFX8X000000X8
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Gaps

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Indels

Length 84;

constructs

Manning SD;

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Method of building bone mass by co-administration of a parathyroid hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound
                                                                                                                                                                Human parathyroid hormone; hPTH; bone mass;
3 (substituted phenoxy)benzo(b)thiophene compound;
bone loss treatment; osteoporosis.
                                                                                                                                 Human parathyroid hormone (hPTH) protein.
                                 AAY02577 standard; protein; 84 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 38; 48pp; English.
                                                                                                                                                                                                                                                                                                                                    98WO-US20848.
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                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   (ELIL ) LILLY
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                                                                                                                                                                                                                                                                   WO9918945-A1
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                                                                AAY02577;
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RESULT 12
AAY02577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is used in the construction of a chimeric protein betagal-1395(FM)PPH84. The enzyme Kex2 protease can be used for excision of a desired protein from a chimeric protein comprising the desired protein and an Arg-Arg. Lys-Arg or Pro-Arg sequence adjacent to the N terminus of the desired protein. It can be specifically used for cleaving this human parathyroid hormone peptide hPH41-84) or peptide hPH41-34) from chimeric proteins such as the beta Gal-1395(FM)PFH84 or CAFPH34. Derivatives of Kex2 protease, and especially Kex2-660 can also cleave such chimeric proteins with high specificity and efficiency even in the absence of urea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the human parathyroid hormone peptide hPTH (residues 1-84). is used in the construction of a chimeric protein betaGal-1398(FM)PI
                                                                                                                                                                                                                                                                  enzyme; chimeric protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted forms of Kex2 protease - useful for cleaving chimeric
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                                                                                                                                                                                                                               Human parathyroid hormone peptide hPTH (residues 1-84).
                                                                                                                                                                                                                                                                                                                                                                 13..44
/note= "cleaved by Kex2 protease"
                                                                                                                                                                                                                                                                                                                                                                                               51.52
/note= "cleaved by Kex2 protease"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yabuta M;
                                                                                                                                                                                                                                                            Kex2 protease; derivative; cleave; yeast;
human; parathyroid hormone peptide; hPTH
                               SHEKSLGEADKADVNVLTKAKSQ 84
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                             AAW25687 standard; Peptide; 84 AA
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                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUNR ) SUNTORY LID.
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                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage-site
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                                                                                                                                                                                               14-APR-1998
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                                         62
                                                                                                                                                              AAW25687;
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Best Local
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                                                                                                                                                                                                                                                                          2 VSEIQLMHNIGKHINSMERVEMLRKKIQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE
The present sequence represents human parathyroid hormone (hPTH). It, and its fragments, are used in the method of the invention. The specification describes a method for building bone mass, comprising
                  coadministration of a parathyroid hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound. The method is used for treatment of bone loss, e.g. in osteoporosis.
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protection, endogenous therapeutic peptide; peptidase, conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                             Length 84;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parathyroid hormone (PTH) related peptide SEQ ID NO:256.
                                                                                                                                                                         Score 417; 'DB 20;
Pred. No. 2.2e-41;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                   SHEKSLGEANKADVNVLTKAKSQ 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB91082 standard; Peptide; 84
                                                                                                                                                                       Query Match
Best Local Similarity 98.8%;
Matches 82; Conservative
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                                                                                                                                    84 AA;
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17-MAY-1999; 10-SEP-1999; 15-OCT-1999;

Bridon DP,

23-NOV-2000

us-09-928-048a-4.rag

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The invention relates to a DNA sequence containing a fragment of the human parathyroxin (hPTH) gene. The invention also relates to splicing strificially synthesised oligodeoxynucleotide chains by PCR and preparing fusion or non-fusion expressed engineering bacteria of recombination protein hPTH through integrating the gene in different expression carriers. This sequence represents a human parathyroxin related protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulating menmalian skin or hair cell proliferation and differentiation by administering nucleic acids encoding peptides derived from N-terminal region of human parathyroid hormone (hPTH) or hPTH-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human parathyroid hormone; hPTH; PTH-related peptide; PTHFP; eczema;
hyperprollferative skin disorder; psoriasis; ichthyosis; skin cancer;
acne; actinic keratosis; alopecia; gene therapy.
                                                                                                                                                                                                                                                   Synthesis and expression of recombinant human parathyroxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.8%; Score 417; DB 23; Best Local Similarity 98.8%; Pred. No. 2.2e-41; Matches 82; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human parathyroid hormone (hPTH) peptide (1-84).
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                                                                                                                                                                                                                                                                                             Disclosure, Fig 1; 16pp; Chinese.
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                                                           13-NOV-2000; 2000CN-0133573
                   13-NOV-2000; 2000CN-0133573
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N-PSDB; AAD37995.
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                                                                                                                                              Huang X, You Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 AA;
                                                                                                                                                                                                              N-PSDB; ABS57477
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                                                                                                  (MEIB/) MEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and malefunido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptides stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VSEIQLMHNLGKHLNSMERVEWLRRKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB9241 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                   Thibaudeau K;
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Pred. No. 2.2e-41;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                 Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG71472 standard; Protein; 84 AA.
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99US-0153406.
99US-0159783.
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Best Local Similarity 98.8%;
Matches 82; Conservative
                                                                                     17-MAY-2000; 2000WO-US13576
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                                                                                                                                                                                                                                                              Ezrin AM,
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    WO200069900-A2
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Sequence

Unidentified

CN1353115-A. 12-JUN-2002.

28-FEB-2003

ABG71472:

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RESULT 14

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Gaps

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Claim 5; Fig 18; 56pp; English.

The invention relates to a method for regulating proliferation or enhancing differentiation of mammalian skin or hair cell. The method involves administering nucleic acids encoding peptides derived from N-terminal region of human parathyroid hormone (hPPH) or hPTH-related peptide (PTHPP). The method is used for inhibiting hyperproliferative ck hait disorders such as psordasis, ichthyosis, acid, acid

Sequence 84 AA;

Query Match 98.8%; Score 417; DB 23; Length 84; Best Local Similarity 98.8%; Pred. No. 2.2e-41; Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 61 SHEKSLGEANKADVNVLTKAKSO 83

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Search completed: October 9, 2003, 08:10:45 Job time: 59.9627 secs

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GenCore version 5.1.6
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October 9, 2003, 08:08:56; Search time 16:1045 Seconds (without alignments) 242.368 Million cell updates/sec US-09-928-048A-4 422 1 VSEIQLMHNIGKHLNSMERV......KSLGEANKADVNVLTKAKSQ 83 Run on:

Title: Perfect score: Sequence:

Scoring table:

127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_41:* Database :

SUMMARIES

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æ	Query	Match	8	97.2	9	85.1	84.1	73.7	i	17.2	۲.	•	•	15.9	•		15.6		15.3				٠	•	14.9	٠	٠		٠	٠	14.7		•	14.5	14.3	
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015811 homo sapien P06618 pseudomonas P35841 desulfovibr P33175 mus musculu 012840 homo sapien P02562 oryctolagus P9474 mycobacteri 090339 cyprinus ca 028641 oryctolagus P02565 gallus gall 015020 homo sapien 031211 staphylococ
ITN1 HUMAN HYIN_PSESS DCRA_DESVH KINN_MOUSE KINN_HUMAN MYSS_RABIT SYR12_WCTU MYSS_CYPCA MYH4_RABIT MYH4_RABIT SYCP_HUMAN MYH3_CHICK SPCP_HUMAN
ਰਕਰਕਰਰਜਰਜ਼ਰ:
1721 4555 668 1027 1032 1084 1172 1938 1938 1940 2390
60 60 60 60 60 60 60 60 60 60 60 60 60 6

ALIGNMENTS

OOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	trathyrin) (PTH) (Parathormor uniata; Vertebrata; Euteleost arrhini; Hominidae; Homo. "B J.T. Jr., Rich A.; "MAS encoding human prepropar 7365-7369(1981). "A. Kronenberg H.M.; "Parathyroid hormone gene."; 2127-2131(1983). "A. Keutmann H.T., Segre G.V orts J.T. "Parathyroid hormone by a new mino-terminal 37 residues of 384-388(1974). G.N., O'Riordan J.L.H., human parathyroid hormone.";
R RA R	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N. O'Riordan J.L.H., Potts J.T. Jr.; (ID) Talmadge R.V., Owen M., Parsons J.A. (eds.); Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundatio
2 2	Carcium regulating noimplies, pp.9-14, Excerpta Medica Foundation, Amsterdam (1975).

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EMBL;
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                                                                                                                                                                                                                                                                                                                                                   Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer Narrestigation of the solution structure of the human parathyroid and molecular dynamics calculations.";

Biochemistry 30:6936-6942(1991).
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                                                                                                                        MEDIINE-75059220; PubMed-4474131; Green E., Niall H.D., Kreqear G.W., van Rietschoten J., Green E., Niall H.D., Kettmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.; Solid-phase synthesis of the biologically active N-terminal 1-34 peride of human parathyroid hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P., "Solution structures of human parathyroid hormone fragments hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypoparathyroidism.";
J. Clin. Invest. 86:1084-1087(1990).
J. Clin. Invest. 86:1084-1087(1990).
J. FUNCTION: PTH ELEVATES CALCIDN LEVEL BY DISSOLVING THE SALTS
BONE AND PREVENTING THEIR ENAL EXCRETION.
-!- DISEASE: Defects in PTH are a cause of familial isolated
hypoparathyroidism (FIH) [MIM:146200].
-!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93345518; PubMed-8344299;
Barden 7.A., Guthbertson R.M.;
"Stabilized NMR structure of human parathyroid hormone(1-34).";
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Riniker B., Rittel W., Stebber P.;
"Syntheais of sequence 1-34 of human parathyroid hormone.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 32-68.
MEDLINE-95318084; PubMed-7797503;
Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A. Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann
                                          Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr. Ar alnosestigation of the amino-terminal sequence of human parathyroid hormone.";
Biochemistry 14:1842-1847(1975).
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Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Mutation of the signal peptide-encoding region of the preproparathyroid hormone gene in familial isolated
                                                                                                                                                                                              Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20090619; PubMed-10623601;
                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 32-65.
MEDLINE-91299748; Pubmed-2069952;
Klaus W., Dieckmann T., Wray V., S
                             MEDLINE-75146516; PubMed-1125201;
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1 VSEIOLMHNLGKHLNSMERVEWLRKKLODVHNFVALGAPLAPRDAGSGRPRKKEDNVLVE 60
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PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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GG; GG:000180; F:peptide hormone; TAS.
GG: GG:0001816; F:peptide hormone; TAS.
GG: GG:000186; P:cell-cell signaling; TAS.
GG: GG:000186; P:induction of apoptosis by hormones; TAS.
GG: GG:0001861; P:induction of apoptosis by hormones; TAS.
InterPro; IPR001815; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
PF01279; Parathyroin_sub.
PF01279; Parathyrhorm_sub.
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Pred. No. 9.4e-39;
1; Mismatches 0; Indels
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63
12861 MW; 849015736A6E5597 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Disease mutation; 3D-structure.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Parathyrold hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARATHYROID HORMONE
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 email to license@isb-sib.ch)
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                              EMBL; J00301; AAA60215.1; -.
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                                                                 CAA01956.1;
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                                                                                 PIR; A19339; PTHU.
PDB; 1HPH; 10-JUL-95.
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                                                   V00597;
A29146;
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1FVY;
send an
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VARIANT
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Genew;
MIM; 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 115;
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PARATHYROID HORMONE.
FC38F77F1C8CFE56 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Parathyrold hormone precursor (Parathyrin) (PTH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%; Score 366; DB 1;
86.7%; Pred. No. 3.5e-33;
tive 6; Mismatches 5.
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                                                                                                                                                                                                           PIR; JC4202; JC4202.
HSSP; P01268; 12MC.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_aub.
Ffan; PF01279; Parathyroid; 1.
ProDom; PP010687; Pthyrhorm_aub.
SMART; SM00087; PTH; 1.
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                                                                                                                                                                                                                                                                                                                                             SMART; SM00087; PTH; 1
PROSITE; PS00335; PARATHYROID; 1.
Hormone; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 115 AA; 12957 MW;
                                                                                                                                                                                  EMBL; U15662; AAA82584.1; -. PIR; JC4202; JC4202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.7*
Matches 72; Conservative
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P01268:
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                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                        Malaivijitnond S., Takenaka O.;
"Nucleotide sequences of parathyroid gene in five species of macaque
                                                                                                                          of Thalland ";
J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
J. FUNCTION: PTH ELEVATES CALCIUM LEVEE BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
J. SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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MEDLINE-95369696; PubMed-7642102;
ROSOI T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
BeWille J.W., Capen C.C.;
"Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone.";
Gene 160:241-243(1995).
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Mammalla; Eutheria; Carnivora; Fissipedia; Canidae; Canis
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97.2%; Score 410; DB 1; Length 115;
Best Local Similarity 95.2%; Pred. No. 5.5e-38;
Matches 79; Conservative 4; Mismatches 0; Indels
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-i- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARATHYROID HORMONE.
8C2500EF24BE5597 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
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InterPro; IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
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31 BY
115 PA
12890 MW;
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Cercopithecinae; Macaca.
NCBL_TaxID-9541;
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                                                                SEQUENCE FROM N.A.
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P52212;
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SEQUENCE FROM N.A.
MEDILNE-80056617; Pubmed-388425;
Kronenberg H.M., NcDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
Potts J.T. Jr., Rich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weaver C.A., Gordon D.F., Kemper B., Introduction by molecular cloning of artifactual inverted sequences at the 5' terminus of the sense strand of bovine parathyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weaver C.A., Gordon D.F., Kemper B.,;
"Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
Mol. Cell. Endocrinol. 28:411-424(1982).
Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                  'Cloning and nucleotide sequence of DNA coding for bovine
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                                                                                                                                                           Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R., Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D., "Synthesis of a biologically active N-terminal tetratriacontapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biochys, Res, Commun. 267:213-220(2000).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                  Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
Isolation and complete nucleotide sequence of the gene for bovine
parathyroid hormone.";
Gene 28:319-329(1984).
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Marx U.C., Adermann R., Bayer P., Forssmann W.-G., Rosch P.;
"Solution structures of human parathyroid hormone fragments
hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
bPTH(1-37).";
                                                                                                                                                                          Cohn D.V.; **The N-terminal amino-acid sequence of bovine proparathyroid
                                                                                                                                                                                                                                                                                                 Nall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F. Arbach G.D., Potts J.T. Jr., The amino acid sequence of bovine parathyroid hormone I."; Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-71063634; PubMed-5275384; Brewer H.B. Jr., Ronan R.; Bovine parathyroid hormone: amino acid sequence."; Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
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V -> G (IN REF. 4).
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PDB; 12WC; 12-MAR-97.
INTECTPO; IPRO01415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
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                                                                                                                                                                                                                                                                                 MEDLINE-71076162; PubMed-5531031;
                MEDLINE-84262483; Pubmed-6086460;
                                                                                                                                           MEDLINE-74142666; Pubmed-4522780;
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EMBL; J00024; AAA30747.1; --
EMBL; K01938; AAA30749.1; --
EMBL; M25082; AAA30748.1; --
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115
106
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                                                                                                                     SEQUENCE OF 26-115.
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SEQUENCE FROM N.A.
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                                                                                                                                              1 VSEIOLMHNLGKHLNSMERVEWLRKKLODVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
                                                                                                                                                                33 VSEIQFWHNLGKHLSSMERVEWLRKKLQDVHNFVALGASIAYRDGSSQRPRKKEDNVLVE 92
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEQUENCE OF 26-115.
MEDIATE=76018954; PubMed=1164500;
Chu L.L.H., Huang W.Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
"Porcine proparathyroid hormone. Identification, blosynthesis, and
partial amino acid sequence.";
Blochemistry 14:3631-3635(1975).
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                                                                                     Score 359; DB 1; Length 115;
Pred. No. 2e-32;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=87316938) PubMed=3628009; Schmelzer H.-J., Gross G., Widera G., Mayer H.; Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat."; Nucleic Acids Res. 15:6740-6740(1987).
                                                                                                                  7; Indels
                                                           12980 MW; 2ED246B348B80710 CRC64;
                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Parathyrold hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                             PRT; 115 AA.
                                                                                                                                                                                                                       93 SHQKSLGEADKADVDVLIKAKPQ 115
                                                                                                                                                                                                       61 SHEKSLGEANKADVNVLTKAKSQ 83
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InterPro; IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SWART; SW00087; PTH; 1.
                                                                                    Query Match
Best Local Similarity 85.5%;
Matches 71; Conservative
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Mammalla; Eutherla;
NCBI_TaxID-9823;
 41
51
53
61
115 AA;
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(See http://www.isb-sib.ch/announce/
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01-ARR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Parathyroid hormone precursor (PTH).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                   PARATHYROID
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or send an email to license@lsb-sib.ch)
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                                                                                               EMBL; S80127; -; NOT_ANNOTATED_CDS.
PIR; A05091; A05091.
HSSP; P01270; 12WB.
                                                                                                                                        Interpro; IPR001415; Parathyrd_hrm.
Interpro; IPR003625; Pthyrhorm_sub.
                                                                                                                                                                                         Probom; PD010687; Pthyrhorm_sub; 1.
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PROSITE; PS00335; PARATHYROID; 1.
Hormone; Signal.
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MEDLINE-89284968; PubMed-3251402;
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                                                                                                                                                                           fam; PF01279; Parathyroid; 1
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                                                                                  EMBL; M54875; AAA57156.
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115 AA;
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                                                                    EMBL;
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                                                                                                                                                                    1 VSEIGLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE-Parathyroid;
Schmelzer H.J., Gross G., Mayer H.;
"Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endocrinology 136:5600-5607(1995).
-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALIS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-!- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.
-!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-84135846; PubMed-6321505; Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.; "Gene encoding parathyroid hormone. Nucleotide sequence of the rat gene and deduced amino acid sequence of rat preproparathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nutley M.T., Parimi S.A., Harrey S.; "Sequence analysis of hypothalamic parathyroid hormone messenger ribonucleic acid.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 32-115 FROM N.A.
STRAIN-Sprague-Dawley, TISSUE-Brain, Liver, and Parathyrold;
MEDLINE-96079910; PubMed-7588314;
                                                                                                      Score 355; DB 1; Length 115;
Pred. No. 5.5e-32;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-87316938; PubMed-3628009;
MEDLINE-87316938; Orloss G., Widera G., Mayer H.;
"Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
                                                             PARATHYROID HORMONE.
9FE8BCDE614BAC16 CRC64;
                                                                                                                                                                                                                                                                                                                                    PTHY_RAI STANDARD; PRT; 115 AA. P04089; Q63473; Clasted)
10.NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                               93 SHQKSLGEADKAAVDVLIKAKPQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dv. Gene Technol. 21:228-229(1984).
                                                                                                                                                                                                                             61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 259:3320-3329(1984).
 PS00335; PARATHYROID; 1
                              25
31.
115
12852 MW;
                                                                                                        84.1%;
84.3%;
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                                                                                       Query Match
Best Local Similarity 84.35,
10, Conservative
                                                                          115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                   Signa
PROSITE;
Hormone;
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                              SIGNAL
PROPEP
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preproparathyroid hormone.";
J. Bone Miner, Res. 3:689-698(1988).
--- FONCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
--- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phasianinae;
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-89219100; PubMed=2710135;
Russell J., Sherwood L.M.;
"Nucleotide sequence of the DNA complementary to avian (chicken)
preproparathyroid hormone mRNA and the deduced sequence of the
hormone precursor.";
                                                                                                                                                                                                       ;
0
                                                                                                                                    Length 115;
                                                                                                                                                                                                12; Indels
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Kronenberg H.M.;
33 V -> I (IN REF. 3).
62 V -> G (IN REF. 3).
12722 MW. .7B434CFCA528B230'CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of cloned cDNAs encoding chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VSBIQIMHNIGKHINSMERVEWIRKKIQDVHNFVALGAPIAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Uttenback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heldelberg J., Sutton G.C., Fleischmann R.D., Eisen J.A., White O.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps

    SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) - AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                              B309D8E772997F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                               ch 41.4%; Score 174.5; DB 1; Similarity 44.7%; Pred. No. 3e-12; 42; Conservative 14; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                PARATHYROID HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 -------SHEKSLGEANKADVNVLTKAK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            824 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diphosphate + L-leucyl-tRNA(Leu).
                                                                                                                                     PIR; A34937; A34937.
HSSP; P01270; 1HFY.
INTECPRO; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                        SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
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31
119 PA
13943 MW;
                                                                                                  EMBL; M31604; AAA49093.1; -. EMBL; M36522; AAB02866.1; -.
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STRAIN-MSB8 / DSM 3109;
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Hormone; Signal
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Best Local S
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4 IQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALG-APLAP-----RDAGSQRPRKKED
                                                                                                                                         TIGREAMS; TIGRO0396; leus_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  retinoblastoma gene product.";
Nature 352:251-254(1991).
-!- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE RETINOBLASTOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., SUBCELLUIAR LOCATION, AND ALTERNATIVE SPLICING. MEDDINE-93205410; PubMed-8455946; Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.; Alternative splicing of the RBPI gene clusters in an internal exon that encodes potential phosphorylation sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Defec-Jones D., Huang P.S., Jones R.E., Haskell K.M., Vuocolo G.A., Hanobik M.G., Huber H.E., Oliff A.; Cloning of cDNAs for cellular proteins that bind to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94020841; Pubmed-8414517;
Fattaey A.R., Helin K., Dembski M.S., Dyson N., Harlow E.,
Vuccolo G.A., Hanobik M.G., Haskell K.M., Oliff A., Defeo-Jones D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RBBI_HUMAN STANDARD; PRT; 1257 AA.
P29314; Q15991; Q15993; Q15993; Q15992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Retinoblastoma-binding protein 1 (RBBP-1).
RBBP1 OR RBB1.
HOMO Saplens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Characterization of the retinoblastoma binding proteins RBP1 and
                                                                                                                                                                                                                                                                                                                          25; Indels 19;
                                                                                                                                                                                                                                                                                             Length 824;
                                                                                                                                                                                                                         "KMSKS" REGION.
ATP (BY SIMILARITY).
7CB0252A76A844EC CRC64;
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-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                        17.2%; Score 72.5; Di
23.3%; Pred. No. 3.7;
:1ve 25; Mismatches
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                                                                                                                                                                                                            "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                        56 NVLVE----SHEKSLGEANKADVNVLTKAK 81
                                                      HARAR; MELONOTO, . . LGU-TRNASYNTIA. IINCEPPO, IPR002302; LGU-TRNA-SYNT. A. IINCEPPO; IPR001412; TRNA-SYNT. I. Pfam; PF00133; TRNA-SYNT. I. PRINTS; PR00985; TRNASYNTIE.
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584 "K
583 AT
95624 MW;
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AE001702; AAD35261.1;
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                                                                                                                                                                                                                                                                                                                        21; Conservative
                                               HAMAP; MF_00049; -; 1.
               PIR; F72408; F72408.
TIGR; TM0168; -.
                                                                                                                                                                                                                                                           824 AA;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 21; Conserv
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dsDNA viruses, no RNA stage; Herpesviridae;
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GLMS_FUSNN
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                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWAss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelab.sib.ch).
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                                                                                                                                                                                                                                                 MIM; 180201; -. GO CONCIOUS; TAS. GO:0005534; C:nucleus; TAS. GO:0005534; C:nucleus; TAS. GO:0005515; F:protein binding activity; TAS. GO: GO:0003700; F:transcription factor activity; TAS. GO: GO:000536; P:transcription from Pol II promoter; TAS. InterPro; IPR001606; ARID. RAID. InterPro; IPR001606; ARID. InterPro; IPR001606; ARID. InterPro; IPR001699; Tudor. Fram; PP01388; ARID; 1. SWART; SM00501; BRIGHT; 1. SWART; SM00504; BRIGHT; 1. SWART; SM00333; TUDOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                             protein; Alternative splicing, RETINOBLASTOMA, PROTEIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142666 MW; F5COABGDGED431DC CRC64;
                                                      IsoId-P29374-3; Sequence-VSP_004371, VSP_004372;
                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform III).
/FTId=VSP_004371.
N -> D (in isoform III).
/FTId=VSP_004372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lsoform II).
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S -> R (IN REF. 2).
K -> V (IN REF. 2).
A -> T (IN REF. 2).
D -> S (IN REF. 3).
IRKYIM -> SENIICL (
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         555 AA
                                Isold-P29374-2; Sequence-VSP_004373;
                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
         IsoId=P29374-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing
                                                                                                                                                                        EMBL, S66427, AAB28543.1; --
EMBL, S57153; AAB25833.1; --
EMBL, S57160; AAB25834.1; --
EMBL, S57162, AAB25835.2; --
PIR, IS8383; IS8383.
Genew, HGNC:9885; RBBP1.
                                                                                                                                                                                                                                                                                                                                                                                           Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity Zoverest Local 19; Conservative
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618 61
653 65
779 77
1178 117
1196 120
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U50 OR KAllR.
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ID UL25_HSV62

AC P52537;

DT 01-OCT-1996

DT 16-OCT-2001

DE VITION Prote

GN U50 OR KAILR

OS Human herpes
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Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Ivanova N., Greckin G., Zhu L.,

Vasieva O., Chu L., Kogan Y., Chaga G., Haselkorn R.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Ronstein M., Kyrpides N., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium

nucleatum strain Arcc 25586.";

J. Bacteriol. 184:2005-2018(2002).

I. FUNCTION: Catalyzes the first step in hexosamine metabolism,

converting fructose-6P into glucosamine-6P using glutamine as a

nitrogen source (By similarity).

-I- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucosamine-fructos-6-phosphate aminotransferase (isomerizing)
(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 LRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEA----NKADVNVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusobacterium nucleatum (subsp. nucleatum).
Bacteria: Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; T44010; T44010.
InterPro; IPR001493; UL25.
Pfam; PF01499; UL25; 1.
SEQUENCE 555 AA; 63830 MW; 68B86590DC4CD2BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    606 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.5%; Score 69.5;
35.4%; Pred. No. 5;
Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF157706; AAB06348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 KADTO 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 KAKSQ 83
                   NCBI_TaxID-36351;
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VSEIQLM-HNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-E] TOR NIG961 / Serotype O1;

MEDLINE-20406633; PubMed-10952301;

Heidelberg J.F., Elsen J.A., Nelson M.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
glutamate + D-glucosamine 6-phosphate.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMILY.
                                                         -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                  GLUTAMINE AMIDOTRANSFERASE.
(GATASE (BY SMILARITY).
ISOMERIZATION FRU-6P (BY SIMILARITY).
D6AE271D4747D5EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
-!- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION COMPLEX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                       IGRFAMS; TIGRO1135; glmS; 1.
ROSITE; PSO0443; GATASE_TYPE_II; 1.
ransferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.1%; Score 68; DB 1; Length 606; 25.6%; Pred. No. 8.1; Live 21; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
ATP-dependent hs1 protease ATP-binding subunit hs1U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 -- HTEALPAGELKHGSIALIEK 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ESHEKSL--GEANKADVNVLTK 79
                                                                                                                                                                                                                  AMAP; MF_00164; -; 1.
nterPro; IPR000583; GATase_2.
nterPro; IPR005855; GlmS.
nterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                            67768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                        EMBL; AE010557; AAL94648.1; -.
                                                                                                                                                                                                                                                                         fam; PF00310; GATASe_2; 1.
fam; PF01380; SIS; 2,
IGRFAMS; TIGR01135; glmS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 25.6
nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           601
606 AA;
                                                                                                                                                                                                                                                                                                                                                     Complete protecme.
                                           SUBFAMILY
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Q9KNQ7;
                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               CT_SITE
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HSLU_VIBCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 HINSMERVEWIRKKLODVHNFVALGAPLAPRDAGSORPRKKEDNVLVESHEKSL--GEAN 70
-1- SUBUNIT: Interacts with halv (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. VIrol. 65:5597-5604(1991).
-!- FUNCTION: VIRION PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
EHV-1 36, EBV BVRP1, HCKY UL77, ILTY ORP2, AND VZV 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-91374623; PubMed-1654455;
Josepha S.F., Ablashi D.V., Salahuddin S.Z., Jagodzinski L.L.,
Wong-Staal F., Gallo R.C.;
"Identification of the human herpesvirus 6 glycoprotein H and
putative large tegument protein genes.";
J. Virol. 65:5597-5604(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 64 ATP (POTENTIAL).
443 AA; 49900 MW; DAE13E82FAB6A38F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human herpesvirus (type 6 / strain GS) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 67; DB 1; 28.8%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chaperone, ATP-binding, Complete proteome NP_BIND 57 64 ATP (POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         interPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR004491; Hsp_HslVU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Betaherpesvirinae, Roseolovirus.
NCBL_TaxID=10369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-001-1996 (Rel. 34, Last sequence-correction (Rel. 40, Last anno Virlon protein USO (Fragment). USO OR LF3.
                                                                                                                                                                                                                                                                               EMBL; AE004333; AAF95815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00382; AAA; 1.
TIGREAMS; TIGR00390; hSlU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; AAA; 1.
                                                                                                                                                                                                                                                                                                       E82046; E82046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 KADVNV 76
                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996
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P52536;
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1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRD---AGSQRPRKKEDNV 57
                                                101 KADAO 105
                     79 KAKSQ 83
                                                                                                                                                                                                      DINB OR CAC0285
                                                                                                                                                                                                                                                Clostridium
                                                                                                                      CLOAB
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                       LRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEA----NKADVNVLT
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                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95266321; PubMed-7747482;
Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Martin M.E., Efstathiou S., Craxcon M., Macaulay H.A.;
"The DNA sequence of human herpesvirus-6: structure, coding content,
and genome evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gompels U.A., Carss A.L., Sun N., Arrand J.R.; Infectivity determinants encoded in a conserved gene block of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  herpesvirus-6.";
DNA Seq. 3:25-39(1992).
-!- FUNCTION: VIRION PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
                                                                                                                                 'n
                                                                                                      Length 378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Indels
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                       BE8B2EF416270AB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63594 MW; BA0C879FF56130D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.8%; Score 66.5; DB 1; 33.8%; Pred. No. 11; ive 11; Mismatches 27;
                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                       (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                15.8%; Score 66.5; D
33.8%; Pred. No. 6.9;
ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-378 FROM N.A. MEDLINE-93091236; Pubmed-1333836;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Betaherpesvirinae; Roseolovirus
                                                                      378 AA; 43459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X83413; CAA58384.1; -- EMBL; X64320; CAA45605.1; -- InterPro; IPR002493; UL25. Pfam; PF01499; UL25; 1.
EMBL; S57509; AAB19777.1; -.
PIR; F56653; F56653.
InterPro; IPR002493; UL25.
Pfam; PF01499; UL25; 1.
NON_TER 378 378
                                                                                                              Local Similarity 33.8% hes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 209:29-51(1995).
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 Virion protein U50.
U50 OR BHRF3.
                                                                                                                                                                                                                               || :|
101 KADAQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Matches 22; Conserv
                                                                                                                                                                                                            79 KAKSQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10370;
                                                                                                                                                                                                                                                                                                                                       01-OCT-1996
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SEQUENCE
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                                                                                                Query Match
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Noelling J., Breton G., Omelchako M.V., Makarova K.S., Zeng Q., Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucallle P., Daly M.J., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucallle P., Daly M.J., Bennett G.W., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostidium accetobutylicum."; "J. Bacteriol. 183:4623-4838(2001).

1. FUNCTION: Poorly processive, error-prone DNA polymerase involved in untargeted mutagenesis. Copies undamaged DNA at stalled replication forks, which arise in vivo from mismatched or mismaligned primer ends. These mismligned primers can be extended by poliv. Exhibits no 3'-5' exonuclease (proofreading) activity. May be involved in translessional synthesis, in conjunction with the beta clamp from polir! (By similarity).

C. CATALYIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EME outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBSTRATE DISCRIMINATION (BY SIMILARITY).
BY STMILARITY.
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
A19826BCBCOD5410 CRC64;
                                                                                                                                                                                                                                                                   Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBUNIT: Monomer (By similarity).
-i- SUBCELULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: BECONGS TO THE DNA POLYMERASE TYPE-Y FAMILY.
-i- SIMILARITY: CORTAINS 1 unuc Gomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Indels

    I- COFACTOR: Binds two magnesium ions (By similarity).

                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase IV (EC 2.7.7.7) (Pol IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
15.6%; Score 66; DB 1
Best Local Similarity 31.0%; Pred. No. 8.2;
Matches 26; Conservative 11; Mismatches
396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; G96934; G96934.
HAMAP: MF_01113; -; 1.
InterPro; IPR001126; UMUC_11ke.
Pfam; PF0817; IMS; 1.
PROSITE; PS50173; UMUC, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE007542; AAK78266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45363 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; Mutator protein;
DOMAIN 5 .192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 1
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-1488;
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g

\$ a

Search completed: October 9, 2003, 08:11:21 Job time: 18:1045 secs

023544 arabidopsis

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65.5
65.5
65.5
65
October 9, 2003, 08:08:56 ; Search time 74.3284 Seconds (without alignments) 288.159 Million cell updates/sec
                                                                                                                422
1 VSEIQLMHNLGKHLNSMERV......KSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                 830525
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                           830525 seqs, 258052604 residues
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                  Minimum DB seq length; 0
Maximum DB seq length; 200000000
                                                                                                       US-09-928-048A-4
                                                                                                                 Perfect score:
                                                                                                                                              Scoring table:
                                                                                                                                                                           Searched:
                                                                                                                            Sednence:
                                                               Run on:
                                                                                                      Title:
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Q97ce4 thermoplasm
Q8w3d7 oryza sativ
Q9shtl arabidopsis
Q8s8b4 arabidopsis
Q8sb4 arabidopsis
Q8n2d8 hom saplen
Q8b2d8 mus musculu
Q8av29 guillardia
Q9av29 guillardia
Q9av29 guillardia
Q9av256 mus musculu
Q9av29 guillardia
Q9av29 guillardia
Q9av29 guillardia
Q9av29 mus musculu
Q9av36 peleonecte
Q8bvv6 mus musculu
Q9vv80 speleonecte
Q8bvv6 mus musculu
Q9vv80 mus musculu
Q8vv80 m

097CE4 0843D7 095HT1 085BH 08H2D2 08H2D2 09PBY4 09AVZ9 0922S6 0922S6 0922S6 0922S6 0922S6

ALIGNMENTS

O13110 gallus gall O9ust0 schizosacch Q98951 gallus gall

013110 Q9UST0 Q98951

Q8IYT6

Q8BXV6 Q9CWX9 Q9NXU3 Q9NXB6 Q9JKB5 Q9PS7 Q9PS77 Q94 Q9NUP4 Q8NEH6

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1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VSEIQLMHNIGKHLNSVERVEWLERKKLQDVHNFIALGAPIFHRDGGSQRPRKKEDNVLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIINE=20082911; PubMed=10613847;
MEDIINE=20082911; PubMed=10613847;
MEDIINE=20082911; PubMed=10613847;
MILLOR Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.;
"A comparative gene map of the horse (Equus caballus).";
"A comparative gene map of the horse (Equus caballus).";
EMBL; AF134233; AAF62347.1;
HSSP; P01270; 1HPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 AA; 9805 MW; 253184EA681A2022 CRC64;
                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Parathyrold hormone (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 368; DB 6; L4
Pred, No. 2.2e-33;
8; Mismatches 5;
                                                                                         86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD010687; Pthyrhorm_sub; 1.
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01279; Parathyrold; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.2%;
84.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.3
Matches 70; Conservative
                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                    Q9N1V0
Q9N1V0;
RESULT 1
Q9N1V0
                                                                                                                                     SO DE RELIER DE LA COMENTA DE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_archeap:*

sp_vertebrate:* sp_rvirus:* sp_bacteriap:*

p_rodent:*

sp_plant:* sp_virus:*

sp_phage:

sp_invertebrate:*

sp_fung1:* sp_human:*

sp_mammal:*

sp_archea:* sp_bacteria:*

Database

sp_mhc:* sp_organelle:*

SUMMARIES

0901v0 equus cabal 090167 fells slive 092016 mus musculu 091y90 peromyscus 091y91 peromyscus 091y91 peromyscus 091y91 peromyscus 091y92 sparus aura 099wc5 staphylococ 08bya2 mus musculu 08by08 staphylococ 08by12 methalosarc

0918E9 0918U2 091Y90 091Y91

79.5

099WC5 Q8BYA2 **08NX08** Q8TJX5

Description

Q9N1VO

Query Match Length DB

Score

Result ပ္

Q81mt1 oryza sativ Q81hc6 oryza sativ O66878 aquifex aeo Q8mrhl drosophila Q9vdc2 drosophila

08LMT1

68.5 67.5 67.5

Q8MRH1

16.8 16.4

ö

63

Gaps

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us-09-928-048a-4.rspt

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1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peromyscus maniculatus (Deer mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
Peromyscus.
                                                                                                                                                                                     Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 84; DB 11; Length 31;
Pred. No. 0.024;
Mismatches 1; Indels
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prince K.L., Dewey M.J.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF382953; AAK63072.1;
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001415; Parathyrd_hrm.
Pfam; PF01279; Parathyrom_sub.
Prom; PF01179; Parathyrorm_sub.
Probom; PF0110697; Pthyrhorm_sub.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                    DA43FABBCB4E2FD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A208B0E772B9B55B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                POTENTIAL.
PARATHYROID HORMONE.
                                                                                                                                                                                 72.7%; Score 307; DB 11;
69.9%; Pred. No. 1.8e-26;
11ve 13; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 AA.
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                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                61 SHEKSLGEANKADVNVLTKAKSQ 83
                 Pfam; PF01279; Parathyroid; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
   InterPro; IPR003625; Pthyrhorm_sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91Y90
Q91Y90;
Q91Y90;
Q91PBC-2001 (TEMBLrel. 19, Create
01-DEC-2001 (TEMBLrel. 19, Last s
01-OCT-2002 (TEMBLrel. 22, Last s
Parathyrold hormone (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TTEMBLEEL. 19, Cree 01-DEC-2001 (TTEMBLEEL. 19, Last 01-OCT-2002 (TTEMBLEEL. 22, Last Parathyroid hormone (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                            1 25 P
32 115 P
115 AA; 12825 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VSEIQLMHNLGKHLNSME 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 AA; 3461 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94,4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 VSEIQLMHNLGKHLASME
                                                                                                                                                                                                                       58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                    Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10042;
                                                                                                                               CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                   Query Match
                                                                                             Signal.
SiGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    091Y91
091Y91;
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     DR X X X E LE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                Felis silvestris catus (Cat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M. "Cloning of the murine gene encoding parathyroid hormone: genomic organization and nucleotide sequence.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Cranjata, Vertebrata, Euteleostomi,
Mammalla, Eutherla, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TOTIBLO R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
"Molecular cloning of feline preproparathyroid hormone.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF309967; AAG30545.1;
HSSP; P01268; 12WC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.8%; Score 358; DB 6; Length 11 larity 83.1%; Pred. No. 3.9e-32; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARATHYROID HORMONE,
80CD557CC6A1A47E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                             ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::||||||:|||:|||:||| ||:||| 93 NHQKSIGEADKADVDVLIKAKSQ 115
                                                                                                                                                                                                                Preproparathyroid hormone precursor.
SHEKSLGEANKADVNVLTKAKSQ 83
                 61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003625; Pthyrhorm_sub-
Pfam, PF01279; Parathyrold; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SMART; SW00087; PTH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001415; Parathyrd hrm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:97799; Pth.
InterPro; IPR001415; Parathyrd_hrm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 25 PC
32 115. P2
115 AA; 12921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hormone precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF066075; AAC99656.1;
HSSP; P01270; 12WB.
                                                                                                                          PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9685;
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SEQUENCE Query Match

Matches

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01-MAY-1999 01-JUN-2002

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0920L6;

RESULT 3 Q9Z0L6

Last sequence update)
Last annotation update)

sea bream)

Created)

us-09-928-048a-4.rspt

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Actinopteryg11; Neopteryg11; Teleoste1; Euteleoste1; Neoteleoste1;
Acanthomorpha; Acanthopteryg11; Percomorpha; Perciformes; Percolde1;
                                                                                                                                                                                                                                                Flanagan J.A., Power D.M., Bendell L.A., Guerreiro P.M., Fuentes Clark M.S., Canario A.V., Danks J.A., Brown B.L., Ingleton P.M.; "Cloning of the cDNA for sea bream (Sparus aurata) parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                  robom; PD013225; PTH_related; 1.
EQUENCE 162 AA; 18722 MW; 6E8D5E07F9E5EDC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.6%; Score 78.5; DB 13;
Best Local Similarity 28.4%; Pred. No. 0.68;
Matches 31; Conservative 11; Mismatches 32;
                                                                                                                                                                                                                                                                                            hormone-related protein.";
Gen. Comp. Endocrinol. 118:373-382(2000).
EMBL; AF197904; AAF79073.1;
                                                                    Parathyrold hormone-related protein.
                                                                                                                                                                                                                                                                                                                                                       interPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003626; PTH_related.
                                                                                                                                                                                                                               MEDLINE-20304721; PubMed-10843788;
                                                                                                                                                                                                                                                                                                                                                                                      fam; PF01279; Parathyroid;
                        01-OCT-2000 (TEMBLED. 15, 01-OCT-2000 (TEMBLED. 15, 01-MAR-2003 (TEMBLED. 23,
                                                                                                 Sparus aurata (Gilthead
                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                            Sparidae; Sparus
                                                                                                                                                                            CBI_TaxID-8175;
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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099WC5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 VSHAQIMHDKGRSLQEFRRRMALHKLLEEVHT-----ANEEAPPVQSRTQTQTFSGN 90
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20314478; PubMed-10854780;
Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
Elgar G., Clark M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic structure and expression of parathyroid hormone-related protein in a teleost, Fugu rubripes."; Gene 250:67-79(2000).
EMBL: AJZ49391; CAB94712.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 163;
                                                                                                                                                                                                                          Score 84; DB 11; Length 31;
Pred. No. 0.024;
0; Mismatches 1; Indels
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                                         Prince K.L., Dewey M.J.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF3812927-3AM63071.1;
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyrold; 1.
ProDom; PD0110687; Pthyrhorm_sub; 1.
PROSITE; PS00335; PARATHYROID; 1.
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3AC5F2C764732278 CRC64;
                                                                                                                                                                                              A208B0E772B9B55B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parathyroid hormone-related protein precursor
                                                                                                                                                                                                                                                                                                                                                                                             163 AA.
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; Pred. No. 0.53;
10; Mismatches
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interPro; IPR001415; Parathyrd.hrm.
interPro; IPR005626; PTH_related.
Pfam; PP01279; Parathyroid; 1.
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                                                                                                                                                                                                                                                                                    1 VSEIQLMHNLGKHLNSME 18
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18698 MW;
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l Similarity 94.4%;
17; Conservative
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Best Local Similarity 27.3%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                           SECUENCE FROM N.A
NCBI_TaxID-42413;
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01-MAR-2003
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Matches
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Length 162;

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1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                             Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kananori M., Matsumaru H., Maruyama A., Murakani H., Hosoyama A., Mutatani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T. Hattori M., Ogasawara N., Hayashi H., Hiramatau K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EANKA-----DVNVLTKAKSQ 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-JUN-2003 (TrEMBLrel. 23, Last annotation update)
1-MAR-2003 (TrEMBLRel. 23, Last annotation update)
1-JUN-2003 (TremBlate)
1-JUN-2003 (TremBlate)
1-JUN-2003 (TremBlate)
1-JUN-2001 (TremBlate)
1-JUN-20
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Staphylococcus aureus (strain N315).
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NCBL_TaxID-158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_centr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 17, Created)
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162 AA

PRT;

PRELIMINARY;

Q918U2 ID Q918U2

RESULT 7

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376 LORMEQIE-----QELKTLKADGVSVAPAQKSSKKPARGIQKSKNAFSMQQIAKVLDKA 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6J; TISSUB-Thymus;
MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the Allysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 LINSMERVEWLRKKI, ODVHNFVALGAPLAPRDAGSORP----RKKEDNVLVESHEKSLGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.3%; Score 73; DB 16; Length 565; Best Local Similarity 29.4%; Pred. No. 12; Matches 20; Conservative 15; Mismatches 23; Indels
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                                                                                                                                                                                                                                                                                                                                          F29A7F07095F02AA CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 23, Last annotation update)
DNA polymerase III gamma and tau subunits.
Staphylococcus aureus (strain MM2).
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InterPro: IPR001270; Chaprnin_clpA/B.
InterPro: IPR000345; CytC_heme_bind.
InterPro: IPR000863; Ratty_acid_BP.
InterPro: IPR000862; Recdomain_Pfam; PF00004; AAA; 1.
PRINTS; PR00300; CLPPROTEASEA.
SMART; PS001300; CLPPROTEASEA.
PROSITE; PS00130; CYTOCHROME_C; 1.
PROSITE; PS00130; CYTOCHROME_C; 1.
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SEQUENCE 565 AA; 63471 MW;
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430 NKADIKLL 437
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Matches 19; Conserv
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DT 01-MA
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OS Staph
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14 INSMERVEWERKKLODVHNFVALGAPLAPRDAGSORP----RKKEDNVLVESHEKSLGEA 69
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MEDLINE—21929760; PubMed=1193238;
MEDLINE—21929760; PubMed=1193238;
FitzHugh W., Calvo S., Engels R., Endrizzi M.G., Macdonald P.,
FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
Allen N., Maylor J., Stange-Thomann N., Dearellano K., Johnson R.,
Linton L., McEwan P., McEernan K., Talamas J., Tirrell A., Ye W.,
Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.
Hedderich R., Ingram—Smith C., Kueytoki J.A.,
Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
Ferry J.G., Jarrell R.F., Jing H., Macario A.J.L., Paulsen I.,
Metchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
Metcalf W.W., Birren B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                   MEDLINE-22040717; Pubmed-12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                 famiamoto K., Hiramatsu K.; "Genome and virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete protecme.
SEQUENCE 565 AA; 63524 MW; 00AFCFDA7A54C6F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
Bacteria; Firmicutes; Bacillales; Staphylococcus NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 29.4%; Pred. No. 20;
Conservative 15; Mismatches 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02274; Amidinotransf; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
                                                                                                                                                                                                               Lancet 359:1819-1827(2002).
EMBL; AP004823; BAB94298.1; -.
InterPro; IPR003959; AAA_ATPase_centr.
                                                                                                                                                                                                                                                                               PR001270; Chaprnin_clpA/B.
PR000345; CytC_heme_bind.
PR000463; Fatty_acid_BP.
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS00214; FABP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interPro; IPR003198; Amidinotransf.
                                                                                                                                                                                                                                                                                                                                           : IPR000862; RFCdomain
                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00300; CLPPROTEASEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and physiological diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||: :|
430 NKADIKLL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 NKADVNVL 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 12:
EMBL; AE011074;
                                                                                                                                                                                              acquired MRSA.
                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                        nterPro
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PD004109; IPP.
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QBLMT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LASRLNLLLPRVSWLRGCSTTAVGQKHQRQVPTEFAVHDPL-----QAHALKEQCILV 54
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.: George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungali C.J., Nunco J., Pacleb J., Paragas V., Park Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 256;
                                                                                               3 EIQLMHNLGKHLNSMERVEWLRKKLQD---VHNFVALGAPLAPRDAG 46
                                      Score 69; DB 17; Length 334;
Pred. No. 18;
                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
Transferase; Complete proteome.
SEQUENCE 334 AA; 37958 MW; 0465FE751248EAB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD004109, TPP_Isomerase, 1,
256 AA; 29755 MW; B817A263391654EA CRC64;
                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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31.1%; Pred. No. 15;
Live 12; Mismatches
                                                             6; Mismatches
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NCBI_TaxID=7227;
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FlyBase; FBGn0038876; CG5919,
InterPro; IPR002667; IPP_isomerase.
InterPro; IPR000086; NUDIX_hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09VDC2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq.
01-0CT-2002 (TrEMBLrel. 22, Last ann
CG5919 protein (GM0827lp).
                                     16.4%;
ilarity 40.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                     PRELIMINARY;
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                                    Query Match
Best Local Similarity
Matches 19, Conserv
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Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                DBMRH1;
                                                                                                                                                                    QBMRH1
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09VDC2
                                                                                                                                              RESULT 12
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RAMERIER DATA CALLEGENER E. BIOLE R. P. ENDRESS C. A. GOCONDE J.D.,
R. MORRIER R. L. LEGENER E. B. BICK R. P. ENDRESS R. R. GOLDER R. P.
R. MORRIER R. L. LEGENER E. B. BICK R. P. ENDRESS R. R. GOLDER R. P.
R. SULTON G. C. MORTHON J. R. Y. YANGHIJ M. D. BANGO C. Champer R. P. GOLDER R. P. SULTON G. C. Champer R. P. GOLDER R. P. MALLON G. R. BANGO C. C. CHAMPER R. P. MALLON G. R. BANGO C. BANGO C. C. CHAMPER R. BOLDER R. P. BERNER R. BOLDER R. P. BERNER R. BOLDER R. R. BOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 INDVALVENLKYNLLSVSQILWARILMCCSRKLE----VRIGHVGFDHLTRLSGSDLVR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VSEIQLMHNLGKHLNSMERVEWLR-----KKLQDVHNFVALG-----APLAPRDAGS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VSEIQLMHNLGKHLNSMERVEWLRKKLOD-VHNFVALGAPLAPRDAGSORPRKKEDNV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              smann V., Hsiao J., Blunt S., Vanaken S.S., Shubum T.V., Yang Q.Q., Haas B.J., Suh B.B., Shubush J., White O., Salzberg S.L., Fraser C.M. Orden 10 BAC OSJNBaQ079813 genomic sequence."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ukaryota, Viridiplantae, Streptóphyta, Embryophyta, Tracheophyta, permatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, nrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 GLPKLKKDLDLVCSPCRHAKMVASSRTPIVSVMTDAPGQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 ORPRKKEDNVLVES---HEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                               Last sequence update)
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; Pred. No. 29;
21; Mismatches
271 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s; Score 67.5; D
i; Pred. No. 21;
19; Mismatches
                                                                                                                                  Putative polyprotein, 3'-partial (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
TRAIN=cv. Nipponbare;
asaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                              Ouyang S:, Liu J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                        Created)
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sativa chromosome 10 BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
29864 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.3%;
Matches 27; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2002) to the EMBL; AC104616; AAM54142.1; Gramene; Q8LMT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 22, (TrEMBLrel. 22, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP004365; BAC05624.1;
Gramene; Q8LHC6; -.
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Best Local Similarity 20.55,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              C.R., Yuan Q., Ouyang
on II L.L., Bera J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
PRELIMINARY;
                                                      01-ocr-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1458E05.24 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eterson J.J.,
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SEQUENCE
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Search completed: October 9, 2003, 08:13 Job time : 77.3284 secs

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TITLE OF INVENTION: STABLLITY ENHANCED VARIANTS OF TITLE OF INVENTION: STABLLITY ENHANCED VARIANTS OF TITLE OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSE: FOLEY & TATATOT SUPPRESSE: FOLEY & TATATOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22313-0299
COMPUTER READABLE FORM:
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STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                9, 2003, 08:08:57; Search time 21.0597 Seconds (without alignments) 166.755 Million cell updates/sec
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/cgn2_6/ptodata/1/laa/backfiles1.pep:*
GenCore version 5.1.6 COPYLIGHT (C) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match 1
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Perfect score:
Sequence:
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					ALIGNMENTS	
KESULT US-10-	KESULT 1 US-10-002-818-2	2				
Sed :	Sequence 2, Application	Applicat	10n US/1000281	001	2818	
GEN	GENERAL INFORMATION:	SZ4/BB RMATION:				•
, AP	PLICANT: (TLE OF IN	Cantor, VENTION:	Thomas I Methods	in.	APPLICANT: Cantor, Thomas L. TITLE OF INVENTION: Methods for Monitoring Therapeutic Su	uppression of Parathyr
H	TITLE OF INVENT	VENTION:	Renal	Pat		Secondary Hyperparathyroidism
	FILE REFERENCE: CURRENT APPLICATION NUMBER	NCE: LICATION	NUMBER	ñ	/10/002,818	
5	CURRENT FILING	ILING DATE:	2001	Ė	-11-02	
8.08	SOFTWARE: MI	Microsoft		000	- ASCII format	
SEQ :	SEQ ID NO 2					
	TYPE: PRT		:			
; US-10	ORGANISM: h 0-002-818-2	human parathyroid hormone 2	rathyroi	Ę	ormone peptide fragment	
Quer Best Matc	y Matcl Local	ভ	98.8%; larity 98.8%; Conservative	***	Score 417; DB 4; Length 8 Pred. No. 1.8e-44; 1: Mismatches 0: Indels	83; (s 0; Gans 0;
δŏ	-	VSEIOLMH	NEGRHENS	ME	**************************************	9
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Q A	1	VSEIGLMH	NEGKHENS	ME	SE I OLMHNLGKHLNSMERVEWLRKKLODVHNFVALGAPLAPRDAGSORPRKKEDNVLVE	SORPRKKEDNVLVE 60
δy	61 8	SHEKSLGEANKADVNVLTKAKSO	ANKADVNV	/LTK	AKSQ 83	
đ	61 8	SHEKSLGE	HEKSLGEADKADVNVLTKAKS	_£	TITITI TRAKSO 83	
RESULT US-07-	SULT 2 -07-863-014-2	~				
; Seq ; Pat	Sequence 2, Application US/07863014 Patent No. 5382658	Applicat 382658	lon US∕0	786	3014	
ав 	GENERAL INFORMATION: APPLICANT: KRONIS,	DRMATION RRONI	₩.	Anne		

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1 VSEIQLMHNLGKHLMSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                               Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SYMPHETIC GENE CODING FOR HUMAN
TITLE OF INVENTION: PARATHYROID HORMONE
TOTHER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAYLD G. CONLIN; DIKE, BRONSTEIN, ROBERIS &
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.8%; Score 417; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,197
FILING DATE:
APPLICATION NUMBER: US/08/016,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER: US/07/765,371
ATORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
REGISTRATION NUMBER: 30,901
                                                                                                                                                                                                                                                                                                                                                    61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                                                                                                                                                                         62 SHEKSLGEADKADVNVLTKAKSQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08689190
Patent No. 5714349
GENERAL INFORMATION:
APPLICANT: FUKUDA, TSUNEHIKO
APPLICANT: OSHIKA, Yuri
APPLICANT: YAMADA, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                            98.88;
98.88;
                                                                                                                                                                                 Ouery Match
Best Local Similarity 98.8%;
Matches 82; Conservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 84 amino acids amino acids
                                                       CHARACTERISTICS
                                                                                                                                  ; MOLECULE TYPE: protein US-08-332-453-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                               amino acid
                                                                                                                   linear
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                  899149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 417; DB 1; Length 84;
Pred. No. 1.8e-44;
                                                   SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863,014
FILING DATE: 19920403
CLASSIFICATION: 530
ATTONNEY/AGENT INPORMATION:
NAME: BENTY Stephen A.
REGISTRATION NUMBER: 29,768
RESTRENCE/DOCKET NUMBER: 16777/163 ALLE
TELEPRANICE: (703)836-9300
TELEPRAN: (703)836-9300
TELEPRAN: (703)883-4109
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,453
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Mismatches
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PPLICANT: BOZZATO, Richard P.
TITLE OF INVENTION: BONE-STIMULATING, NO
TITLE OF INVENTION: PARATHYROID HORMONE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Sulte 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,680
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SHEKSLGEANKADVNVLTKAKSQ 83
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5599792
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
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Best Local Similarity 98.8%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                    linear
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1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                      2 VSEIQLMHNIGKHLNSMERVEWIRKKIQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
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                                                                                                                                                                                                                                                                                                                       APPLICANT: SUZUKI, Yuji
APPLICANT: YABUTA, Masayuki
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF SECRETORY KEX2
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 84;
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98.8%; Pred. No. 1.8e-44;
iive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 8-073217
FILING DATE: 04 MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 8-352580
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/805,918
FILING DATE: 04-MAR-1997
                                                                                                      61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                           62 SHEKSLGEADKADVNVLTKAKSQ 84
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                                                                                                                                                                                                                                   Sequence 3, Application US/08805918 Patent No. 5885821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            Poyofumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 98.8
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meuth, Donna M.
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; MOLECULE TYPE: peptide
US-08-805-918-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                           MAGOTA,
MASUDA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Alexandria
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                                                                                                                                                                                                                  US-08-805-918-3
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                                                                            1 VSEIQLMHNLGKHLNSMERVEWLRRKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE
                               Gaps
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Pred. No. 1.8e-44;
1; Mismatches 0; Indels
Best Local Similarity 98.8%; Pred. No. 1.8e-44; Matches 82; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          APPLICANT: NISHIMURA, Osamu
APPLICANT: KUBIYAMA, Masato
APPLICANT: KUGYMA, NO. 5861284uyuki
APPLICANT: FUKUDA, Tunabliko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-PEB-1991
FILING DATE: 18-OCT-1991
ATTORNEY-AGENT INPORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34 --
TELECOMMUNICATION
TELECOMMUNICATION
TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,231
                                                                                                                             61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                               62 SHEKSLGEADKADVNVLTKAKSQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 02711/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
                                                                                                                                                                                                                                                        Sequence 9, Application US/08835231 Patent No. 5861284 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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98.84;
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-835-231-9
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.8
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
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Sequence 1, Application US/10002818
Patent No. 6524788
GENERAL INFORMATION:
APPLICANT: Cantor, Thomas L.
ATILLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathy
TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VSEIQLMHNIGKHLNSMERVEWIRKKLQDVHNFVALGAPLAFRDAGSGRPRKKEDNVLVE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application PC/TUS9515800
GENERAL INFORMATION:
APPLICANT: BIOMEDIASKA, INC.
TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING
TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRICTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           Score 417; DB 4; Length 84;
Pred. No. 1.8e-44;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: human parathyroid hormone peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Merchant & Gould STREET: 3100 Norwest Center, 90 S. 7th Street CITY: Minneapolis
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/002,818
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Microsoft Word 2000 - ASCII format
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/15800
FILING DATE: 07-DEC-1995
CLASSIFICATION:
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APPLICATION NUMBER: 08/350,530.
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 SHEKSLGEADKADVNVLTKAKSQ 84
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98.8%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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Best Local Similarity 98.88
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 84 amino acids
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                                                                                                                               APPLICANT: KORINAMA, Massico
APPLICANT: KORAMA, No. 6887806uyuki
APPLICANT: KORAMA, No. 6887806uyuki
APPLICANT: FUKUNA, TSUNDALIKO
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 417; DB 3;
Pred. No. 1.8e-44;
1; Mismatches 0;
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SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 0/000,000, PILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SHEKSLGEANKADVNVLTKAKSQ 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
                                                 Sequence 9, Application US/09108661
Patent No. 6287806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: 617-523-3400
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98.8%;
                                                                                         GENERAL INFORMATION:
APPLICANT: NISHIMURA, OSAMU
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Best Local Similarity 98.89
Matches 82; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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single

STRANDEDNESS

linear

MOLECULE TYPE: peptide HYPOTHETICAL: NO

RESULT 8 US-10-002-818-1 S

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0; Gaps

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Franco
Use of Parathormone, Its Biologically
Active Fragments and Correlated Peptides, for The Pre
Pharmaceutical Compositions Useful for The Treatment
                                                                                      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                   2 VSEIQLMHNIGKHINSMERVEWIRKKLODVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61
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97.6%; Score 412; DB 2; Length 84
Best Local Similarity 97.6%; Pred. No. 7.5e-44;
Matches 81; Conservative 2; Mismatches 0; Indels
                                          Indels
          Best Local Similarity 97.6%; Pred. No. 7.5e-44;
Matches 81; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,726
FILING DATE: 05-APR-1995
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/02755
FILING DATE: 08-OCT-1993
APPLICATION NUMBER: PCT/EP93
APPLICATION NUMBER: MI-92A002331
FILING DATE: 09-OCT-1992
ATPORNEY AGENT INFORMATION:
RESISTRATION NUMBER: 34,402
RESISTRATION NUMBER: 34,402
RESISTRATION NUMBER: 34,402
RESISTRATION NUMBER: 31,11/1300
                                                                                                                                                                                        61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                  62 SHEKSLGEADKADVDVLTKAKSQ 84
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Patent No. 5880093
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: BAGNOLI, Franco
TITLE OF INVENTION: Que of Para
TITLE OF INVENTION: Active Frag
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1 Broadway
CITY: New York
STATE: N
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-411-726-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10004
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                                                                                                                                                                                                                                                                                                                                           US-08-411-726-1
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                                                                                                                                                                                                                          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                       2 VSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
STREET: 699 Prince Street
                                                                                                                           Score 417; DB 5; Length 84;
Pred. No. 1.8e-44;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.6%; Score 412; DB 2; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : NAME/KEY: Protein

: LOCATION: 1.84

: OTHER INFORMATION: /note= "84 amino acid PTH"

US-08-142-5518-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-UTW-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-CCT-1992
ATTONNEY,FAGENT INPORMATION:
NAME: SWISS, GEFAIL F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKTE NUMBER: 000324-010
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ 10 NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 aning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                              61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                                                                                                                                                        62 SHEKSLGEADKADVNVLTKAKSQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
                                                                                                                           Query Match

Best Local Similarity 98.8%;
Matches 82; Conservative
; ANTI-SENSE; NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
PCT-US95-15800-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22313
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US-08-142-551B-1
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Gaps

RESULT 12

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STORMARE: Patentin Pales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08733446 Patent No. 5856138
                                                                                                                                                                             NAME: MULTAY, Robert B.
REGISTRATION NUMBER: 22,890
REFERENCE/DOCKET UNDERS: 901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.2%;
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        (202) 887-035
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.03
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                  84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FUKUDA, TSUNG
TITLE OF INVENTION: PROL
IUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         TELEX: 440142
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-07-773-098-2
       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                       linear
                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                 FILING DATE: 1
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                                                                                                                                                                                                                                                                                                                                                                                  POPOLOGY:
                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VSEIQLMHULGKHLINSMERVEWERRKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                       APPLICANT: SINDREY, Dennis R.
TITLE OF INVENTION: ESSENTIALLY PURE HUMAN PARATHYROID
TITLE OF INVENTION: HORMONE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Armstrong, Nikaido, Marmelstein, Kubovcik
ADDRESSEE: Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES AS TITLE OF INVENTION: OSTEOPOROTIC CONTROL AGENTS NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 407; DB 1; L
Pred. No. 3.1e-43;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Murray
1725 K Street, N.W., Suite 1000
                                                                                                                                            SEE: Foley & Lardner: 1800 Diagonal Road, Suite 500 Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington D.C.
Y: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 SHEKSLGEADKANYDVLTKAKSO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07773098 Patent No. 5317010 GENERAL INFORMATION:
Sequence 1, Application US/07707114
Patent No. 5208041
                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISSTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 96.4%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PANG, Peter K.T. APPLICANT: JIE, Shan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 84 amino acids
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US
FILING DATE: 19910523
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                   GENERAL INFORMATION:
APPLICANT: SINDRE
                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
CLONE: hPTH
                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                              ADDRESSEE:
STREET: 180
                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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HUMAN PARATHYROID HORMONE MUTEINS AND
PRODUCTION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                            Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
SOFTWARE: Patentin Release #1.0, Version #1.25
AURENT APPLICATION DATA:
AUSTICATION UNMER: US/07/773,098
FILING DATE: 19911010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.25
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Pred. No. 2.1e-38;
4; Mismatches 6
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us-09-928-048a-4.rai

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                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 6.7e-38;
1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Armstrong, Nikaido, Marmelstein, Kubovcik &
                                                                                                                                                                                                                                      mutation
8 Xaa-Leu, Ile, Val, Phe, Tyr, Trp or Met,
18 Xaa-Leu, Ile, Val, Phe, Tyr, Trp or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: PANG, Peter K.T.
APPLICANT: TANG, Peter K.T.
APPLICANT: TIE, Shan
TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES AS
TITLE OF INVENTION: OSTEOPOROTIC CONTROL AGENTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEN PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Murray
STREET: 1725 K Street, N.W., Suite 1000
CITY: Washington D.C.
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/773,098
FILING DATE: 19911010
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MULTAY, RODETE B.
REGISTRATION NUMBER: 22,890
REFERENCE/DOCKET NUMBER: 901930
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: allocati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SHEKSLGEANKADVNVLTKAKSQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 SHEKSLGEADKADVNVLTKAKSO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/07773098
Patent No. 5317010
                                                                                                                                                                                                                                                                                              34 Xaa-Cys or Phe,
37 Xaa-Cys or Leu,
41 Xaa-Cys or Leu,
                                                                                                                                                                                                                                                                                                                                                                                                           86.3%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (202) 659-2930
(202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.04
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 440142
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                LOCATION: 41 Xaa-Cys o IDENTIFICATION METHOD:
                                                                                                                                                                                                   MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                        LOCATION:
LOCATION:
LOCATION:
LOCATION:
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Sequence 6, Appl Sequence 16, Appl Sequence 20, Appl Sequence 6, Appl Sequence 1, Appl Sequence 2, Appl Sequence 5, Appli Sequence 5, Appli

Sequence 17

Sequence

Sequence Sequence Sequence

l, App Appli Appl Appli

Sequence 15, Appl Sequence 4, Appl Sequence 14, Ap Sequence 1, Appl Sequence 9, Appl Sequence 9, Appl

Appl

Sequence 11, Sequence 5, A Sequence 3, A Sequence 5, A Sequence 5, A Sequence 7, A Sequence 7, A Sequence 13,

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1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE
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Patent No. US20020160945A1

GENERAL INFORMATION:

APPLICANT: Cartor. Thomas

TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE

TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS

FILE REFERENCE: 5321-2000.18/09/928,047B

CURRENT APPLICATION NUMBER: US/09/928,047B

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 8

SOSTWARE: FASTSEQ for Windows Version 4.0
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5 US-10-215-770-2

1 US-09-843-221A-11

5 US-09-928-0478-8

0 US-09-928-0478-3

2 US-09-928-048A-7

2 US-09-928-048A-7

2 US-09-928-048A-7

1 US-09-843-221A-13

US-09-843-221A-14

US-09-843-221A-15

US-09-843-221A-16

US-09-928-0478-6

US-09-928-121A-161

US-09-928-121A-161

US-09-928-121A-161

US-09-928-121A-161

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US-10-361-928-5

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Pred. No. 2.4e-43;
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US-09-928-048A-4
Sequence 4, Application US/09928048A
Publication No. US20030138858A1
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llarity 100.0%; P
Conservative 0;
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ORGANISM: Homo sapiens
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Best Local Similarity
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     US-09-928-047B-1
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US-09-928-0478-2

US-09-843-221A-10

US-09-898-398-1

US-09-898-398-1

US-09-898-398-1

US-09-898-398-1

US-09-898-398-1

US-09-843-221A-12

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CURRENT APPLICATION NUMBER: US/09/928,048A CURRENT FILING DATE: 2000-08-10 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
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                                                                                                                                             TYPE: PRT
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              APPLICANT: Scantibodies Laboratory, Inc.
APPLICANT: Cartor, Thomas L.
TITLE OF INVENTION: METHORS AND DEVICES FOR DIRECT
TITLE OF INVENTION: METHORS AND DEVICES FOR DIRECT
TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
FILE REFERENCE: 5321-20015.00
CURRENT APPLICATION NUMBER: US/09/928,048A
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 4
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APPLICANT: CARLOR, Thomas L.
TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
FITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
FILE REFERENCE: 53221-20015.00
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APPLICANT: CARLOT, THOMAS
TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPROSIS
FILE REPERBENCE: 53221-20002.00
CURRENT APPLICATION NUMBER: US/09/928,047B
CURRENT FILING DATE: 2001-08-10
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Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.4e-43;
tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/224,446
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 83; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo saptens
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TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
FILE REFERENCE: 53221-20002.00
CURRENT APPLICATION NUMBER: US/09/928,047B
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/224,446
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TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/215,770
CURRENT PILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US 60/224,446
PRIOR PILICATION NUMBER: US 60/224,447
PRIOR FILING DATE: 2000-08-10
                                                             Indels
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  100.0%; Score 422; DB 12;
100.0%; Pred, No. 2.4e-43;
ative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                    62 SHEKSLGEANKADVNVLTKAKSQ 84
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10215770 Publication No. US20030087822A1 GENERAL INFORMATION:
Query Match
Best Local Similarity 100.0
Matches 83; Conservative
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APPLICANT: Yankovsky, N. K.
APPLICANT: KOZLOV, A. P.
APPLICANT: KOZLOV, A. P.
APPLICANT: LODAShev, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequ
                                                                                                                                                                                                                                                             1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                                                                                                                                                                                     1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09898398
Publication No. US20030082179A1
Publication No. US20030082179A1
SERENAL INFORMATION:
APPLICANT: Hutchison, James Scott
TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
FILE REFERENCE: A1713
CURRENT PAPLICATION NUMBER: US/09/898,398
CURRENT FILING DATE: 2001-07-03
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                                                                                                                                                                       Score 417; DB 11; Length 84;
Pred. No. 9.8e-43;
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Pred. No. 9.8e-43;
1; Mismatches 0;
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CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PATENTIN VEXESION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SHEKSLGEANKADVNVLTKAKSQ
                                                                                                                                                                Query Match
Best Local Similarity 98.8%;
Matches 82; Conservative
           SOFTWARE: Patentin version 3.1
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Best Local Similarity 98.8%;
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-898-398-1
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US-09-843-221A-10
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                               SEQ ID NO 10
LENGTH: 84
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APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID ITTLE OF INVENTION: RELATED PROTEIN
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                                                                                                                                                                                                                                                                            1 SELQLMHNILGKHLINSMERVEWLRKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVES 60
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                                                                                                                                                                                                                                                    2 SEIQLMHNLGKHLNSMERVEWLRKKLODVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES
                                                                                                                                                                Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sato, Masahiko
TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
FILE REFERENCE: X-11480
CURRENT APPLICATION UNMBER: US/09/169,786B
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,800
EARLIER FILING DATE: 1997-10-14
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                                                                                                                                                           Score 418; DB 10,
Pred. No. 7 2e-43;
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Pred. No. 9.8e-43;
1; Mismatches 0;
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99.1%; Score 418; DB
Best Local Similarity 100.0%; Pred. No. 7.2
Matches 82; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/266,673
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/214,860
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
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Publication No. US20030039654A1
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Best Local Similarity 98.8%;
Matches 82; Conservative
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APPLICANT: KOSTENUIK, PAUL
                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-2
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LENGTH: 84
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Length 78;

DB 11;

Score 395;

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RPPLICANT: LIU, CHUAN-FA
RPPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
ITLE OF INVENTION: RELATED PROTEIN
ILE REFERENCE: A-665B
                                                                                     1 VSEIQIMHNIGKHINSMERVEWIRKKIQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                                                                                                                   6 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
FILE REFERENCE: 5321-20002.00
CURRENT APPLICATION NUMBER: US/09/928,047B
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-08-10
         Length 115;
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Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 78; Conservative 0; Mismatches 0;
Ouery Match

Best Local Similarity 98.8%; Pred. No. 1.4e-42;
Matches 82; Conservative 1; Mismatches 0;
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- SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 78
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                                                                                                                                                                             61 SHEKSLGEANKADVNVLTKAKSQ 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/200,053
PRIOR FILING DATE: 2000-04-27
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RIOR APPLICATION NUMBER: 60/266,673
RIOR FILING DATE: 2001-02-06
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FILING DATE: 2000-06-28
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SEQ ID NO 12
LENGTH: 78
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US-09-928-047B-4
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; ORGANISM: HOM
US-09-843-221A-12
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                                             Gaps
                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10215770; Publication No. US20030087822a1; GENERAL INFORMATION:
APPLICANT: CANTON: DARATHYROID HORMONE ANTAGONISTS AND USES TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES; FILE REFERENCE: 53221-20002.20; CURRENT APPLICATION NUMBER: US/10/215,770; CURRENT FILING DATE: 2002-12-16; PRIOR APPLICATION NUMBER: US 60/224,446; PRIOR FILING DATE: 2000-08-10; PRIOR FILING DATE: 2000-08-10; PRIOR FILING DATE: 2000-08-10; PRIOR FILING DATE: 2000-08-10
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1.4e-36;
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APPLICANT: HANADA, TOSHIRO
APPLICANT: SHIRO, MINORU
APPLICANT: SHIRO, MINORU
APPLICANT: KOBATAKE, SHINZO
TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
FULE REPERENCE: SS966(702B)
CURRENT APPLICATION NUMBER: US/09/879,257A
CURRENT FILING DATE: 2001-06-12
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Pred. No. 9.5e-36;
                       4e-40;
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Pred. No. 1.4e-
6; Mismatches
                     Pred. No. 4e-4
1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGIH: 84
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Patent No. US20020081690A1
                                                                                                                                                             86.7%;
Query Match
Best Local Similarity 98.7%;
Matches 77; Conservative
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85.5%;
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SOFTWARE: Patentin Ver.
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Best Local Similarity
Matches 72; Conserva
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Best Local Similarity
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US-10-215-770-3
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1 VSEIQLMHNLGKHLNSMERVEWLRRKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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                                                       2 VSEIQFWHNLGKHLSSMERVEWLRKKLQDVHNFVALGASIAYRDGSSQRPRKKEDNVLVE 61
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                                                                                                                                                                                                                                Sequence 4, Application US/10215770

Fublication No. US20030087822A1

GENERAL INFORMATION:
TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
TITLE OF INVENTION: THEREOF

FILE REFERENCE: 5221-20002.20

CURRENT APPLICATION NUMBER: US/10/215,770

CURRENT APPLICATION NUMBER: US/10/215,770

FRIOR RILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 6

SOFTWARE FRALESEQ for Windows Version 4.0
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Pred, No. 9.5e-36;
5; Mismatches 7;
   Mismatches
                                                                                                         61 SHEKSLGEANKADVNVLTKAKSO 83
                                                                                                                            62 SHQKSLGEADKADVDVLIKAKPQ 84
 71; Conservative
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Best Local Similarity 85.5
Matches 71; Conservative
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; LENGTH: 84
; TYPE: PRT
; ORGANISM: Bovine
US-10-215-770-4
Matches
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Search completed: October 9, 2003, 08:19:28 Job time: 155:851 secs

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Human parathyroid

Leu8 hPTH (7-84) Human parathyroid

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Oxidation resistan

Stability-enhanced Stability-enhanced Stability-enhanced Stability-enhanced Stability-enhanced Stability-enhanced

Title: Perfect score:

Sequence:

protein

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Run on:

Scoring table:

Searched:

Minimum DB. Maximum DB

Database

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Differentiating between normal parathyroid function and hyperparathyroidism comprises determining and comparing whole parathyroid hormone, parathyroid hormone inhibitory peptide fragment and/or total parathyroid hormone levels -
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                                             AAR3085
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26-JUN-1999;
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/SIDS1/gcgdata/geneseqy_geneseqp_embl/AA1991_DAT:*
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253
1 FVALGAPLAPRDAGSQRPRK......KSLGEANKADVNVLTKAKSQ
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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT-
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries

    protein search, using sw model

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ABG74237
ABG74233
AABG7465
ABG74231
ABG74230
AABG74230
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Gapop 10.0 , Gapext 0.5
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Parathyrold hormone; PTH; cyclase activating parathyrold hormone CAP; cyclase inhibiting parathyrold hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium; PTH28-84.
                                           1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                               Human parathyroid hormone-based CIP, PTH28-84 #2.
                                                                                                                                                                     ABG74237 standard; peptide; 57
                                                                                                                                                                                                                                                  (first entry)
     Conservative
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   51;
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                                                                                                                                                                                                             ABG74237;
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                                                                                    between a person having substantially normal parathyroid function and having hyperparathyroidism. The method comprises determining and comparing at least two of the following parameters: whole parathyroid hormone level, parathyroid hormone inhibitory peptide fragment level and total parathyroid hormone level. The method is used for monitoring (treatments of) parathyroid related bone disease and the effects of
                                   The present sequence represents a fragment of human parathyroid hormone (PTH), comprising residues 34-84, which functions as a PTH antagonist. The specification describes a method for differentiating
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parathyrold hormone; PTH; cyclase activating parathyrold hormone; CAP; cyclase inhibiting parathyrold hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium; PTH3-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide
                                                                                                                                                                                                                                                                                                                                                           1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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100.0%; Pred. No. 9.5e-27;
ive 0; Mismatches 0;
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Pred. No. 9.5e-27;
                                                                                                                                                                                                       therapeutic treatment for hyperparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human parathyroid hormone-based CIP, PTH3-84.
Disclosure; Page 43; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG74232 standard; peptide; 51 AA.
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                                                                                                                                                                                                                                                                                                  Similarity
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The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PTH, which regulates extracellular calcium levels) antagonist activity to reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PTH2-84, PTH3-84 and PTH28-84 (appearing as ABG74230 Note: This peptide (SEQ ID 8) is included in the sequence listing but is not referred to anywhere else in the specification. However it does represents PTH amino acids 28-84 (unlike ABG74233 which is referred to as represents 28-84 (unlike ABG74233 which is referred to as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide .
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10-AUG-2001; 2001US-0928047.
                                                                                10-AUG-2000; 2000US-224446P.
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Matches 51; Conserv
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Homo saplens.

31-OCT-2002

Cantor TL;

16-APR-2003

Human

ABG74233;

us-09-928-048a-5.rag

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hormone (PTH), comprising residues 3.84, which functions as a PTH antagonist. The specification describes a method for differentiating between a person having substantially normal parathyroid function and having hyperparathyroidsm. The method comprises determining and comparing at least two of the following parameters: whole parathyroid hormone level. The method is used for monitoring and total parathyroid hormone inhibitory peptide fragment level and total parathyroid hormone level. The method is used for monitoring (treatments of) parathyroid related bone disease and the effects of therapeutic treatment for hyperparathyroidism.
                                                                                                                                                                                                                                                                               Differentiating between normal parathyroid function and hyperparathyroidism comprises determining and comparing whole parathyroid hormone, parathyroid hormone inhibitory peptide fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a fragment of human parathyroid
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100.0%; Pred. No. 1.7e-26;
.1ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               total parathyroid hormone levels
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 42-43; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG74231 standard; peptide; 82
                                                                                                                                                                              (SCAN-) SCANTIBODIES LAB INC
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                                                13-JAN-2000; 2000WO-US00855
                                                                                                      99US-0231422
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Best Local Similarity 100.0
Matches 51; Conservative
                                                                                                                                                                                                                              WPI; 2000-476147/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 AA;
                                                                                                   14-JAN-1999;
26-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
20-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone peptide (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PIH, which regulates extracellular calcium levels) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity to reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PTH2-84, PTH3-84 and PTH28-84 (appearing as ABG74230 -ABG74233). The present sequence is the CIP PTH28-84.

Note: This peptide is referred to in the specification as PTH28-34 but actually represents amino acids 7-84 of PTH. It is therefore unclear whether this peptide (SEQ ID 4) or the peptide appearing as ABG74237 (Which does represent amino acids 28-84 of PTH) is actually intended to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                   Parathyrold hormone; PTH; cyclase activating parathyrold hormone; CAP; cyclase inhibiting parathyrold hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium; PTH28-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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                                                                                     parathyroid hormone-based CIP, PTH28-84 #1.
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100.0%; Pred. No. 1.6e-26;
.ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 4; 8pp; English
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                                        (first entry)
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nes 51; Conserv
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be claimed

Sequence

Query Match

Best Loc Matches

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Gaps

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Length 82; Indels Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide

WPI; 2003-209227/20.

WO200042437-A1

Homo sapiens

AAB07465;

AAB07465 RESULT

21 83

Claim 1;

Sequence

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substantially normal parathyroid function and having hyperparathyroidism. The method comprises determining and comparing at least two of the following parameters: whole parathyroid hormone level, parathyroid hormone inhibitory peptide fragment level and total parathyroid hormone level. The method is used for monitoring (treatments of) parathyroid related bone disease and the effects of therapeutic treatment for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Differentiating between normal parathyroid function and hyperparathyroidism comprises determining and comparing whole parathyroid hormone, parathyroid hormone inhibitory peptide fragment
                                                                                                                                                                                                                                                                                                                            Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents a human parathyroid hormone (PTH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fragments of PTH function as PTH antagonists. The specification describes a method for differentiating between a person having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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                              33 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 253; DB 21;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                Amino acid sequence of human parathyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        levels
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                                                                                                                                                    AAB07464 standard; protein; 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAB INC
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99US-0344639.
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                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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26-JUN-1999;
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                                                                    peptide
                                       The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone peptide (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PTH, which regulates extracellular calcium levels) antagonist activity to reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PTH2-84, PTH34-84, and PTH3-8-84 (appearing as ABG7423). The present sequence is the CIP PTH34-84.
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                                                                                                                                                                                                                                                                                                                                                                                                       82
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                                                                                                                                                                                                                                                                                                                                                                                   Length 83;
                                                                                                                                                                                                                                                                                82:
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Pred. No. 1.7e-26;
Mismatches 0;
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Pred. No. 1.7e-26;
Mismatches 0;
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Best Local Similarity 100.0%; Pi
Matches 51; Conservative 0;
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ilarity 100.0%;
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Page 3; 8pp;
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Best Local Similarity
Matches 51; Conserv
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Homo saplens.

Cantor IL;

16-APR-2003

ABG74230;

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Gaps

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Length 84; Indels Parathyroid hormone; PTH; cyclase activating parathyroid hormone;

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Gaps

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Indels

Sequence

Cantor TL;

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The sequences given in AAW08103-07 represent fragments of human parathroad hormone (PTH) Which were used as Xaa34 in the generic sequence given in AAW08102. Peptides based on the generic sequence are human PTH (1-34) derivative peptides. They have potent cAMP-producing activity and be been formation activity. They may be used in treatment of bone diseases including osteoporosis, hypoparathyroidism, hypertension and climacteric disturbance. The peptides are low in toxicity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Codons 29-84 are degenerate in the usage frequency favoured by E.coli or yeast. Codons 1-28 (see AAQ11617) are designed to contain adenine rich codons. The sequence is prepd. from eight oilgonuclectides (4 on each strand). A plasmid contg. the complete sequence expresses PTH with an improved yield. The sequence expresses PTH with an improved yield. The is a blood (Updated on 25-MRR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSO 51
                                                                                              New parathyroid hormone derivs. - useful in treatment of bone diseases, hypoparathyroidism and hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 98.0%; Score 248; DB 18; Length 51; 1 Similarity 98.0%; Pred. No. 4.5e-26; 50; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                           Claim 3; Page 39; 42pp; English
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Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AA;
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03-JUL-1991
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AAR11732
                * # X # # X 8 X D D D D D D D D X 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone peptide (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PTH, which regulates extracellular calcium levels) antagonist activity to reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PPH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as ABG74230-ABG74233). The present sequence is full length human PTH, the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide.
CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 100.0%; Score 253; DB 24; Similarity 100.0%; Pred. No. 1.8e-26; 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukuda T, Habashita J, Nakagawa S, Taketomi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human parathyroid hormone residues 34-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ABG74233). The present sequence 1s fuupon which the CIP peptides are based.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW08107 standard; peptide; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 8pp; English.
                                                                                                                                                                                                                                        10-AUG-2001; 2001US-0928047.
                                                                                                                                                                                                                                                                                             10-AUG-2000; 2000US-22446P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96EP-0109475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       West Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 AA;
                                                                                                                                  US2002160945-A1.
                                                                             Homo sapiens
                                                                                                                                                                                      31-OCT-2002,
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Sequence

Query Match

Matches

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AAW08107;

AAW08107 RESULT

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Gaps

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Sequence

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The sequence is that of mutated human parathyroid hormone (hPTH) (7-84) where Met8 is substd. by Leu. It has higher stability, enhanced activity and improved absorption by tissues. It can act as a PTH antigonist and can be used as a therapeutic agent for hypercalcaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human parathyrold hormone; hPTH; PTH related peptide; PTHTP; eczema; hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer; acne; actinic keratosis; alopecia; gene therapy.
                                                                              Human parathyroid hormone, hPTH; antagonist; hypoparathyroidism;
hypercalcaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FVALGAPLAPRDAGSÓRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human parathyrold mutein(s) - useful for treating osteoporosis, hypoparathyroldism, hyperparathyroldism, hypercalcaemia, hypertension etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 248; DB 14;
Pred. No. 7.6e-26;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and hyperparathyroidism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                       Location/Qualiflers
                                                                                                                                                                                   /note= "Met -> Leu"
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                                                                                                                                                                                                                                                                                                     91JP-0198056.
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ilarity 98.0%;
Conservative
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       (updated)
(first entry)
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                                                 Leu8 hPTH (7-84) mutein.
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       25-MAR-2003
09-JUN-1993
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26-JUN-1992;
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Best Local Simi
Matches 50;
                                                                                                                         Synthetic.
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Region
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AAE23725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a human parathyroid hormone (hPTH) peptide lacking 6 hPTH N-terminal amino acids. The peptide can have higher stability, enhanced activity and improved absorption by tissues. It can act as a PTH antagonist and can be used as a therapeutic agent for hypercalcaemia and hyperparathyroidism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                          Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
                                                                                                  5 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSIGEADKADVNVLTKAKSQ 55
                                                                                         51
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                                                                                    1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHERSLGEANKADVNVLTKAKSQ
                                 Length 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human parathyroid mutein(s) - useful for treating osteoporosis, hypoparathyroidism, hyperparathyroidism, hypercalcaemia, hypertension etc.
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Pred. No. 7.6e-26;
1; Mismatches 0;
                              DB 12;
                             Score 248; DB 12
Pred. No. 5e-26;
1; Mismatches
                                                                                                                                                                                                                                                                                             hPTH mutein lacking 6 N-terminal amino acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 7; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR30859 standard; Protein; 78 AA.
                                                                                                                                                                                         AAR30852 standard; Protein; 78
                          Query Match
Best Local Similarity 98.0%;
Matches 50; Conservative
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92JP-0169713.
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Best Local Similarity 98.0%;
Matches 50; Conservative
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                                                                                                                                                                                                                                                     (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-060187/08.
55 AA;
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                                                                                                                                                                                                                                                                                                                                           hypercalcaemia
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09-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-AUG-1992;
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26-JUN-1992;
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Pukuda T;

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Synthetic.

AAR30852;

RESULT 12 AAR30852

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11-APR-2002

AAR30859;

RESULT 13 AAR30859

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Length 78; Indels 27-APR-2000; 28-JUN-2000;

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differentiation by administering nucleic acids encoding peptides derived from N-terminal region of human parathyroid hormone (hPTH) or hPTH-related protein
                                                                                                                Claim 35; Fig 15; 56pp; English.
       05-OCT-2001; 2001WO-US31082
                   06-OCT-2000; 2000US-238134P
                                                          WPI; 2002-452304/48.
                                 (HOLI/) HOLICK M F.
                                                                  N-PSDB; AAD37995
                                              tolick MF;
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ch 98.0%; 1 Similarity 98.0%; 50; Conservative Query Match Best Local Similarity Best Loca Matches ç

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AAU73024 standard; Peptide; 78 AA. (first entry) 12-MAR-2002 AAU73024; RESULT 15 AAU73024

Parathyroid hormone PTH/PTHrP modulating domain #6.

PTHTP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody, calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone; osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone; breast cancer; prostate cancer; cachexia; anorexia; osteoporosis; Paget's disease; osteomyelitis; osteonecrosis; bone cell death; Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus; theumatoid arthritis; periodontal disease; alopecia; fracture repair; parathyroid hormone, PTH; parathyroid hormone-related protein bone resorption inhibitor; immunoglobulin G; IgG Gaucher's

Homo saptens

WO200181415-A2

01-NOV-2001

27-APR-2001; 2001WO-US13528

The invention relates to a method for regulating proliferation or enhancing differentiation of mammalian skin or hair cell. The method involves administering nucleic acids encoding peptides derived from Involves administering nucleic acids encoding peptides derived from N-terminal region of human parathyroid hormone (hPTH) or hPTH-related peptide (PTHP). The method is used for inhibiting hyperproliferative skin disorders such as sportasts, tothhyosis, eccens, acne, actinic regrowth. It is useful for stimulating cell growth, rejuvenating aged skin, preventing skin winkles, enables, treating skin winkles, enabancing wound chealing, stimulating hair growth, treating or preventing female or male pattern baldness, for treating chemotherapy induced alopecta and also for stimulating epidermal cell growth or hair follicle cell growth. The method is also used in gene therapy. ô Score 248; DB 23; Length 78; Pred. No. 7.6e-26; 1; Mismatches 0; Indels 0; Indels 78 AA; Sequence

Gaps 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSO 51

The invention relates to a composition (I) comprising modulators of parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHP) which comprises a PTH/PTHP modulating domain and a vehicle. (I) comprises a PTH agonist optionally with a bone resorption inhibitor, such as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates, cestrogen receptor modulators and tibolone is useful for treating osteopenia. (I) is useful for therapeutic and prophylactic purposes. Antagonists of PTH receptor are useful in treating primary and secondary hyperthyroidism, hypercalcaemia, tumour metastases, particularly breast and prostate cancer, cachaita and anorexia, osteopenia, including various forms of osteoporosis, Paget's disease of bone, osteomyelitis, osteonecrosis or bone cell death, associated with firmment of the page of the pa disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid arthritis, periodontal disease and alopecia. PTH receptor agonists are useful as therapeutic agents in conditions including fracture repair (including healing of non-union fractures), osteopenia, including various forms of osteoperosis, AA0730181 represent parathyroid hormone and parathyroid hormone related protein (PTH/PTHIP) modulators and related amino acid sequences of the invention. Gaps Composition, useful for treating osteopenia, comprises parathyroid hormone and parathyroid hormone-related protein receptor modulators ö Length 78; Indels 98.0%; Score 248; DB 23; 98.0%; Pred. No. 7.6e-26; ive 1; Mismatches 0; Disclosure; Page 26; 107pp; English. Lacey DL 2001US-266673P. 2001US-0843221. Query Match
Best Local Similarity 98.0v
Best Local Similarity 56.0v
Conservative Liu C, WPI; 2002-066435/09. (AMGE-) AMGEN INC 78 AA; Kostenuik P, 26-APR-2001; 06-FEB-2001; Sequence

1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51 ò

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October 9, 2003, 08:08:56; Search time 18.2687 Seconds (without alignments) 268.471 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1: pir1:*
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3: pir3:*
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Database :

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	ALIGNMENTS
	RESULT 1 PTHU
	parathyroid hormone precursor [validated] - human
	NyAlternate names: proparathyroid hormone C:Species: Homo gapiens (man)
	C;Accession: Aly339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94· R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts
	Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
	A/IILLe: Nucleotide sequence of the human parathyroid normone gene. A/Reference number: A19339; MUID:83169834; PMID:6220408
	A; Accession: A19339
	A;Molecule type: DNA A;Residues: 1-115 <vas></vas>
	A;Cross-references: GB:J00301; NID:g190702; PIDN:AAA60215.1; PID:g190704
	R; Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.
	A:Title: Purification of meprin from human kidney and its role in parathyroid how
	A; Reference number: S53790; MUID:95225988; PMID:7710697
	A: MOTEONIA COLO
	A. Residues: 'X', 31, X', 35-46,65-84,105-110 < XAM>
	Ridacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
*	Nacture 489, 132-137, 1374 A:Title: Structural analysis of human proparathyroid hormone by a new microsequer
	A:Reference number: A93169; MUID:74174967; PMID:4833516
	A. Accession: A93169
_	A, Molecule type: protein A, Residines: 26-37 < TAC>
	Richard O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautt
_	ArTitle: Isolation and characterization of two biologically active O-glycosylated
	ation. A:Reference number: S21199: MUID:92209518: PMID:1555591
	A;Accession: S21199
	A; Molecule type: protein
	A.Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycos
	R; Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan,
	Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974
	A;Title: 'ne amino-acid sequence or tre amino-terminal 3/ residues or numan parat A;Reference number: A93789: MUTD:74111656: PMID:4521809
	A, Accession: A93789
	A; Molecule type: protein
	A. M.
	A; Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal res
	A; Accession: A93783
_	A; Molecule type: protein

J.W.; Car

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1995 #sequence_revision 27-Oct-1995 #text_change 16-Jul-1999
                                                                                                                  L.K.; Groene,
                                                                                                        RiRosol, T.J.; Steinmeyer, C.L.; McCauley, Gene 160, 241-243, 1995
A;Tille: Sequences of the cDNAs encoding ca A;Reference number: JC4201; MUID:95369696; A;Accession: JC4202
                    familiaris (dog)
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ses 42; Conserv
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A; Residues: 1-115 <ROS>
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A; Residues: 1-115 <WEA>
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Matches
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A.Residues: 75-100 (KRE2)
R.Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J. Roppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A.Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum A.Title: Solid-phase synthesis of residues 32-65
A.Reference number: Asl660; MOID:75059220; PMID:4444131
A.Solid-phase annotation: Synthesis of residues 32-65
A.Note: the biologically active amino-terminal 34 residues of parathyroid hormone were star renal adenylate cyclase assay and with the bovine hormone's active region in the chic R.Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel, Helv. Chim. Acta 56, 470-473, 1973
A.Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A.Reference number: A91635; MUID:73227467; PMID:4721748
A.Solid-physiologically synthesis of residues 32-65
A.Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroidectomized rate caused a distinct increase in plasma calcium level
                          Note: this sequence was determined by sequenator and mass spectroscopic identification Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.M.; Hendy, G.N.; O'Riordan, J.L.
M., and Parsons, J.A., eds., pp.9-
                                                                                                                                      parathyroid hormone.
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Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
Reference number: 138342; MUID:82150870; PMID:6950381
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                                                                                                                                                                                                                   A Molecule type: protein
A Residues: 52-75 «KE3>
R Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts
Blochemistry 17, 5723-5729, 1978
A Title: Complete amino acid sequence of human parathyroid hormone.
A Reference number: A90426; MUID: 79082855; PMID: 728431
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                                                                                                                            A:Title: A reinvestigation of the amino-terminal sequence of A:Reference number: A90387; MUID:75146516; PMID:1125201
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R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, in Calcium-regulating Hormones, Talmadge, R.V., Owen, 34,Reference number: A94410
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Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>
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Pred. No. 7e-23;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atus: translated from GB/EMBL/DDBJ
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98.0%;
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Cross-references: GDB:119522;
Map position: 11p15.2-11p15.1
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                                                               RiKeutmann, H.T.; Niall, H.D
Blochemistry 14, 1842-1847,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A: Molecule type: protein A: Residues: 61-106, 'D', 10
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Residues: 1-115 <RES>
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      hormone-related pro
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A/Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Cross-references: GB:V00106; GB:J00023; NID:g84; PIDN:CAA23439.1; PID:g85
A;Note: the authors translated the codon GAA for residue 50 as Gly
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.;
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974
A;Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone.
A;Reference number: A93793; MUID:74142666; PMID:4522780
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775; 145976; A01534
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                                                                                                                                                   A;Cross-references: GB:U15662; NID:q558915; PIDN:AAA82584.1; PID:q558916 Cs. Superfamily: parathyroid hormone; parathyroid hormone homology C;Keywords: hormone 
E:1.31/Domain: signal sequence *status predicted <SIG>
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C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change
C;Accession: A24849; A9385; A93793; A91648; A93773; 145975; 145
R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper,
Gene 28, 319-329, 1984
A;Title: Isolation and complete nucleotide sequence of the gene
A;Reference number: A24949; MUID:84262483; PMID:6086460
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                                                                                                                                                                                                                                                                         F:30-64/Domain: parathyroid hormone homology <PTH>F:32-115/Product: parathyroid hormone #status predicted <MAT>
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canine parathyroid
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R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979
A;Title: Cloning and nucleotide sequence of DNA coding for bA;Reference number: A93835; MUID:80056617; PMID:388425
A;Accession: A93835
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A; Residues: 26-115 < GRAM>
R; Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; I
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970
A; Title: The amino acid sequence of bovine parathyzoid
A; Reference number: A91648; MUID:71076162; PMID:5531031
                                                                                                                                                                                                                                                                                                                                                                               Score 206; DB 2;
Pred. No. 8.5e-18;
5; Mismatches 4.
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Residues: 32-115 KNIA>
Brewer Jr., H.B.; Ronan, R.
Troc. Natl. Acad. Sci. U.S.A.
Filtle: Bovine parathyroid ho
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A:Residues: 32-115 <BRE>
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hormone precursor

parathyroid

RESULT 2

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A;Molecule type: protein
M:Residues: 32-109 <SAD-
R;Residues: 32-109 <SAD-
R;Brewer Jr. , H.B.; Falrwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A. Title: Recent studies on the chemistry of human, bowine and porcine parathyroid
A;Reference number: A90030; MUID:74173303; PMID:4598526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adv. Gene Technol. 21, 228-229, 1984
A; Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormon
A; Reference number: 151851
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C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
C;Accession: A05091; A26806
E;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Cham. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
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C;Date: 26-Jul-1996 *sequence_revision 26-Jul-1996 *text_change 16-Jul-1999
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A;Title: Nucleotide sequence of a full-length cDNA clone encoding preprop A;Reference number: A26806; MUID:B7316938; PMID:3628009
A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A/Cross-references: GB:M54875, NID:g601932; PIDN:AAA57156.1; PID:g601933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSO 51
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0
                                                                                                                                                                                                            A.Contents: annotation
C.Superfamily: parathyroid hormone; parathyroid hormone homology
C.Keywords: calcium; hormone; parathyroid gland
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-31/Domain: propeptide #status experimental <PRO>
F:30-64/Domain: parathyroid hormone homology <PTH>
                                                                                                                                                                                                                                                                                                                                                                                                           F;32-115/Product: parathyroid hormone #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 115;
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C;Superfamily: parathyroid hormone; parathyroid hormone homology
E;20-54/Domain: parathyroid hormone homology <PTH>
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Pred. No. 2.4e-16;
4; Mismatches 7;
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Pred. No. 2.9e-12;
B; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parathyroid hormone - rat (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.2%;
Best Local Similarity 62.7%;
Matches 32; Conservative E
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ilarity 78.4%;
Conservative
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Best Local Similarity
Matches 40; Conserv
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A; Residues: 1-115 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: I51851
R; Schmelzer, H.
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A; Reference number: A93776; MUID:71091588; PMID:4322265
A; Contents: annotation; synthesis of residues 32-65
A; Note: the synthetion peptide was active in vivo and in vitro
B; Brower Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
An. J. Med. 56, 759-766, 1974
A; Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormon A; Reference number: A90030; MUID:74173303; PMID:4598526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arathyroid hormone precursor - pig
Species: Sus scrofa domestic (domestic pig)
19ate: 24-Apr-1984 sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
1Accession: B26806; A90390; A90376; A01535
1. Mayer, H. J.; Gross, G.; Widera, G.; Mayer, H.
1. Schmelzer, H. J.; Gross, G.; Widera, G.; Mayer, H.
1. Itle: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
1. Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
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A; Residues: 26-115 <CHU>
R; Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr.,
Blochemistry 13, 194-1999, 1974
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                                                                                                                                                                                                                                                           R;Weaver, C.A.; Gordon, D.F.

Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981

Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981

A;Title: Introduction by molecular cloning of artifactual inverted sequences at A;Reference number: 145975; MUID:82037785; PMID:6170060

A;Accession: 145975
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A; Residues: 1-115 <SCH>
A; Cross-references: N. 115 <SCH>
A; Cross-references: 1. 115 <SCH>
A; Cross-references: 1. 115 <SCH>
B; Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A; Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partification a; A90390; MUID: 76018954; PMID: 1164500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNĀ
A;Residues: 1-115 <WE3>
A;Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645
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4; Mismatches
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Local Similarity 80.4%;
les 41; Conservative
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A; Residues: 1-115 <WE2>
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Length 283;

DB 2;

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   Query Match
Best Local
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C.Accession: H86803
R.Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001
A.; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A; Reference number: A86625; WUID:21235186; PMID:11337471
A.Accession: H86803
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Mol. Endocrinol. 3, 325-331, 1989
Mol. Endocrinol. 3, 325-331, 1989
Molitle: Nuclectide sequence of the DNA complementary to avian (chicken) preproparathyro
A;Reference number: A34937; MUID:89219100; PMID:2710135
A;Accession: A34937
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Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.
Bone Miner. Res. 3, 689-689, 1988
Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone. Reference number: 150411; MUID:89284968; PMID:3251402
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                                 Cross-references: GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA29192.1; PID:g56003
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.;Molecule type: DNA
.;Residues: 1-283 <STO>
.;Cross.references: GB.AE005176; PID:g12724421; PIDN:AAK05530.1; GSPDB:GN00146
.;Gross.references: Grain IL1403
.;Genetics: ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parathyroid hormone precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C;Accession: A34937; ISO411
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                                                            C;Genetics: 29/3
A;Introns: 29/3
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>
                                                                                                                                                                                                                         Length 115;
                                                                                                                                                                                                                     Score 160; DB 2; Length 11
Pred. No. 3.2e-12;
8; Mismatches 11; Indels
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mes 32; Conservative
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Residues: 1-119 <RUS>
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Residues: 1-119 <KHO>
A; Residues: 1-115 <SCH>
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Ribevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, P.; Wedler, H.; Mancroft, I.; Bent, R.; Goodman, H.; Dean, C.; Bergkamp, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Fuster S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puster Erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, C.; Chalwatzis, N.
Aritile: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidop A; Reference number: A71407
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 17-May-1996 sequence_revision 17-May-1996 *text_change 19-Apr-2002
C;Accession: 138055; JH0154; S12459; S09332; A30220; S49478
R;Jullian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Stedr Eur. J. Blochem. 230, 1001-1006, 1995
A;Title: Characterization of a human perinatal myosin heavy-chain transcript. A;Reference number: 138055; MuID:95324556; PMID:7601129
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1937 <RES>
A; Cross-references: EMBL: Z38133; NID: 9558668; PIDN: CAA86293.1; PID: 9558669
R; Karsch-Mizrachi, I.; Feghall, R.; Shows, T.B.; Leinwand, L.A.
B; Karsch-Mizrachi, I.; Feghall, R.; Shows, T.B.; Leinwand, L.A.
A; Title: Generation of a full-length human perinatal myosin heavy-chain-encoding
A; Reference number: J40154; MUID: 90323631; PMID: 2373371
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA , A;Residues: 1-487 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                  probable Ste20-like kinase - Arabidopsis thaliana (Scotsa) Arabidopsis thaliana (Mouse-ear cress) Arabidopsis thaliana (Mouse-ear cress) A.Variety: columbia A.Variety: columbia Sequence_revision 03-Aug-1998 #text_change 16-Dec:1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:297336; NID:q2244788; PID:e326893; PID:g2244804
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 487;
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 APRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                 8; Mismatches .15;
                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
25.1%; Score 63.5; DB 2;
Best Local Similarity 30.2%; Pred. No. 7.1;
Matches 13; Conservative 12; Mismatches 11;
                                                                                                                                                      15 SQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKS
Score 65; DB 2
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, January 1989
A; Reference number: $12458
A; Accession: $12459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4COP9-4G3845
C; Superfamily: protein kinase homology
F;13-293/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-14,'A',16-859 <KAR>
A; Cross·references: GB:Y00821
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: skeletal
                                                                           Conservative
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Thu Oct

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C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C; Species: 
                                                           - Staphylococcus aureus (stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Status: preliminary
A; Molecule type: DNA
A; Residues: 1-565 < KUR>
A; Residues: 1-565 < KUR>
A; Cross-references: GB:BA000018; PID:g13700368; PIDN:BAB41666.1; GSPDB:GN00149
A; Experimental source: strain N315
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ALGAPLAPRDAGSQRP----RKKEDNYLVESHEKSLGEANKADVNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: dnaX
C;Superfamily: DNA-directed DNA polymerase III gamma chain
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C;Superfamily: varicella-zoster virus gene 34 protein
                                          polymerase III gamma and tau subunits [imported]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.1%; Score 61; DB 2; 31.9%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virion protein [imported] - human herpesvirus 6
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Best Local Similarity 42.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.9%
Matches . 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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J. Cell Biol. 108, 1791-1797, 1989
A;Title: Molecular genetic characterization of a developmentally regulated human perinat
A;Reference number: A30220; MUD:89234168; PMID:2715179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 860-969, 'Q', 971-1246,'H',1248-1260,'G',1262-1296,'Q',1298-1503,'AH',1506-184
A.Cross-references: GB:Y00821; NID:g34863; PIDN:CAA68757.1; PID:g34864
                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein HI1405 - Haemophilus influenzae (strain Rd KW20)
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Date: 18 Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-oct-1999
C; Accession: A64028
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P.; Godayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Reference number: A64020, MUD:95350630; PMID:7542800
A; Accession: A64020
A; A
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C; Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide
E; 91-769/Domain: myosin motor domain homology <a href="https://domain.myosin.motor.domain.homology">https://domain.myosin.motor.domain.homology</a> <a href="https://domain.myosin.motor.domain.homology">https://domain.myosin.motor.domain.homology</a> <a href="https://domain.myosin.motor.domain.homology">https://domain.myosin.motor.domain.homology</a> <a href="https://domain.homology.domain.homology">https://domain.homology</a> <a href="https://domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domain.homology.domai
A; Residues: $62-1071,'N',1073-1250,'DGG',1253-1376,'NM',1379-1913,'D',1915-1937 <BOB>
A; Cross-references: EMBL:X31592; NID:g29465; PIDN:CAB35941.1; PID:g29466
A; Cross-references: clone gtMnC-F
B; Experimental source: clone gtMnC-F
B; Bober, E.; Buchberger-Seidl, A; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
Eur. J. Blochem. 189, 55-65, 1990
A; Title: Identification of three developmentally controlled isoforms of human myosin h
A; Reference number: S09331; MUID:90235862; PMID:1691980
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24.3%; Score 61.5; DB 2; Length 366;
Best Local Similarity 35.6%; Pred. No. 9.1;
Matches 16; Conservative 10; Mismatches 18; Indels
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Pred. No. 35;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross - references: GDB:125267; OMIM:160741
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Matches

ò g ä

myosin heavy chain, skeletal muscle - rabbit (fragment) C; Species: Oryctolagus cuniculus (domestic rabbit)

RESULT 14 A02985

RESULT 12

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); Accession: S24348
(; Moore, L.A.; Arrizubleta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
(; Mol. Biol. 255, 1145-1151, 1992
1; Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
1; Reference number: S24348; MUID:92309413; PMID:1377278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myodin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragmen C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-555 <MOO>
A; Cross-references: EMBL:N74085
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: ATP; colled coll; muscle contraction; skeletal muscle; thick filament
31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 13-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                            A;Note: this fragment is from the heavy meromyosin subfragment. 2
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; colled coil; muscle; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 2; Length 955;
Pred. No. 38;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                            Score 60; DB 2; Length 258;
Pred. No. 9.6;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9, 2003, 08:14:29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                         Query Match 23.7%;
Best Local Similarity 42.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.7%;
Best Local Similarity 42.4%;
Matches 14; Conservative
                                                      R;Capony, J.P.; Elzinga, M.
Biophys. J. 33, 148a, 1981
A;Reference number: A02985
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60.23.7 1937 1 MYH8_HUMAN 60.23.7 1935 1 MYSS_CYPCA 60.23.7 1935 1 MYSS_CYPCA 60.23.7 1936 1 MYSS_CYPCA 60.23.7 1940 1 MYH4_ANA 60.23.7 1 MYH4_ANA 60.23.7 1 MYH4_ANA 60.23.7 1 M</td><td>Score Match Length DB ID 248 98.0 115 1 PTHY_HUMAN 241 95.3 115 1 PTHY_HUMAN 242 95.3 115 1 PTHY_BOVIN 194 76.7 115 1 PTHY_BOVIN 68.5 27.1 119 1 PTHY_BOVIN 60.5 27.1 119 1 PTHY_BOVIN 60.5 27.1 119 1 PTHY_RAT 60.2 27.1 119 1 PTHY_RAT 60.2 23.7 1084 1 MYSS_RABIT 60.2 23.7 1084 1 MYSS_CYPCA 60.2 23.7 1084 1 MYSS_CYPCA 60.2 23.7 1938 1 MYHA_CHICK 58.5 23.1 57.1 1940 1 MYHA_CHICK 58.5 23.1 57.1 1940 1 MYHA_CHICK 58.5 22.9 1935 1 MYHA_CHICK 59.5 22.9 1935 1 MYHA_CHICK 50.5 22.7 378 1 UL2S_HSV6U 50.5 22.7 378 1 UL2S_HSV6U 50.5 22.7 378 1 UL2S_HSV6U 50.5 22.7 378 1 ULS_HSV6U 60.5 23.7 378 1 ULS</td></td<></td></td> | Query Query SCOTE Match Length DB ID 248 98.0 115 1 PTHY_HUMAN 241 95.3 115 1 PTHY_ACRA 206 81.4 115 1 PTHY_ACRA 194 76.7 115 1 PTHY_PIG 68.5 27.1 115 1 PTHY_PIG 68.5 27.1 119 1 PTHY_PIG 68.5 27.1 119 1 PTHY_PIG 61.5 24.3 366 1 XBO5_HARIN 60.5 23.9 55.5 1 UL2S_HNY6Z P24537 60 23.7 1 035 1 MYSS_CYPCA 020339 60 23.7 1938 1 MYHA_RABIT 020841 60 23.7 1938 1 MYHA_RABIT 028641 60 23.7 1940 1 WYHA_RABIT P02565 58.5 23.1 1 WYHA_RABIT P02862 | Query Query Score Match Length DB ID 248 98.0 115 I PTHY_HOWAN P01270 241 95.3 115 I PTH_AACPA Q9x135 266 81.4 115 I PTH_AACPA Q9x135 194 76.7 115 I PTHY_BOTH P01269 160 63.2 115 I PTHY_RAT P01269 68.5 27.1 119 I PTHY_CHCK P1357 61.5 27.1 119 I PTHY_CHCK P1357 61.5 24.9 1937 I MYHB_HONAN P1353 61.5 23.9 555 1 UL25_HSVG P02562 60.5 23.7 1084 I MYSS_CYPCA Q90339 60 23.7 1940 I MYHB_ARAIT P02565 60 23.7 1940 I MYHB_ARAIT P02565 60 23.7 1940 I MYHB_ARAIT P02565 60 23.7 1940 I MYHB_ARAIT | Querry Querry 248 98.0 115 1 PTHY_HOMAN P01270 241 95.3 115 1 PTHY_ACPA Q9x435 206 81.4 115 1 PTHY_ACPA P02212 194 76.7 115 1 PTHY_PIG P01269 160 63.2 115 1 PTHY_PIG P04089 68.5 27.1 119 1 PTHY_PIG P04089 68.5 27.1 119 1 PTHY_PIG P04089 61.5 24.3 366 1 PMAP P16 P13535 61.5 24.3 366 1 PWB P04089 P04389 61.5 24.3 366 1 PWB P02567 P02567 60 23.7 1084 1 WYSS_CYPCA P02567 60 23.7 1938 1 WYHA_RABIT P02565 58 22.9 465 1 | Query Query Score Match Length DB ID 248 98.0 115 1 PTHY_HUMAN P01270 241 95.3 115 1 PTHY_CANPA P01270 206 81.4 115 1 PTHY_CANPA P01269 194 76.7 115 1 PTHY_PIG P01269 160 63.2 115 1 PTHY_PIG P01269 68.5 27.1 119 1 PTHY_CHICK P04089 61.5 24.9 1937 1 WYHY_CHICK P15743 60.5 23.1 1937 1 WYHY_CHICK P25733 60.5 23.9 10125_HSV62 P44180 60 23.7 1034 1 WYHA_CRAT P02563 60 23.7 1936 1 WYHA_RABIT P02563 60 23.7 1940 1 WYHA_RABIT P04460 58 22.9 465 1 WYHA_RABIT P04460 58 22.9 465 1 WYHA_RABIT P04460 | Querry Querry 248 98.0 115 1 PTHY_HOWAN P01270 241 95.3 115 1 PTHY_AACPA Q9x435 266 81.4 115 1 PTHY_AACPA
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PTHY_EAVE 61.5 24.9 1937 1 MYH8_HOWAN 60.5 23.7 1946 1 MXSS_CYPCA 60 23.7 1948 1 MXSS_CYPCA 60 23.7 1948 1 MXSS_CYPCA 60 23.7 1940 1 MYH4_RABIT 61.5 22.9 1935 1 MYH7_HOWAN 62.2 1 1935 1 MYH7_HOWAN 62.2 1935 1 MYH7_HOWAN 62.2 1935 1 MYH7_RAT 63 22.9 1935 1 MYH7_RAT 64 22.9 1935 1 MYH7_RAT 65 22.9 1935 1 MYH7_RAT 66 22.9 1935 1 MYH7_RAT 67 26 26 26 26 26 26 26 26 26 26 26 26 26</td> <td>Score Match Length DB ID 248 98.0 115 1 PTHY_HOWAN 241 95.3 115 1 PTHY_HOWAN 242 95.3 115 1 PTHY_ROUTH 243 96.0 115 1 PTHY_ROUTH 244 115 1 PTHY_ROUTH 245 27.1 115 1 PTHY_PIG 66.5 27.1 119 1 PTHY_RUT 66.5 27.1 119 1 PTHY_RUT 67.2 24.9 1937 1 MYHB_HUMAN 61.5 24.9 1937 1 MYHB_HUMAN 60.2 27.7 1938 1 MYHB_HUMAN 60.2 27.7 1938 1 MYHB_RMIT 60.2 27.9 1935 1 MYHB_RMIT 60.2 27.9 1935 1 MYHB_RMIT 60.2 27.9 1935 1 MYHT_RMIN 60.2 27.9 1935 1 M</td> <td>Score Match Length DB ID 248 98.0 115 1 PTHY_HOWAN 241 95.3 115 1 PTHY_ACPA 206 115 1 PTHY_ACPA 206 115 1 PTHY_ACPA 207 115 1 PTHY_ACPA 208 115 1 PTHY_ACPA 208 115 1 PTHY_ACPA 208 27.1 119 1 PTHY_PIG 20.3 24.9 1937 1 MYHB_HOWAN 60.5 23.4 366 1 YROS_HARIN 60.5 23.4 366 1 YROS_HARIN 60.2 23.7 1084 1 MYSS_CRABIT 60 23.7 1084 1 MYSS_CRABIT 60 23.7 1938 1 MYHB_CHICK 58 22.9 1935 1 MYHB_CHICK 58 22.9 1935 1 MYHB_CHICK 58 22.9 1935 1 MYHT_PIG 60 23.7 1940 1 MYHB_CHICK 60 23.7 1940 1 MYHB_CHICK 61 23.7 1940 1 MYHB_CHICK 62 23.7 1940 1 MYHB_CHICK 63 22.9 1935 1 MYHT_PIG 64 22.9 1935 1 MYHT_PIG 65 22.9 1935 1 MYHT_PIG 66 22.7 378 1 MYHT_RABIT 67 22.9 1935 1 MYHT_PIG 68 22.9 1935 1 MYHT_PIG 68 22.9 1935 1 MYHT_PIG 69 22.7 378 1 MYHT_RABIT 60 22.8 1</td> <td>Score Match Length DB ID 248 98.0 115 1 PTHY_HOWAN 241 95.3 115 1 PTHY_AGTA 266 81.4 115 1 PTHY_AGTA 194 76.7 115 1 PTHY_EANT 194 76.7 115 1 PTHY_ENT 195 27.1 119 1 PTHY_ENT 68.5 27.1 119 1 PTHY_ENT 68.5 27.1 119 1 PTHY_ENT 60.2 23.7 1937 1 MYH8_HOWAN 60.2 23.7 1935 1 MYSS_RABIT 60.2 23.7 1935 1 MYSS_RABIT 60.2 23.7 1935 1 MYH4_RABIT 60.2 23.7 1940 1 MYH4_RABIT 60.2 23.7 1935 1 MYH4_RABIT 60.2 23.7 1935 1 MYH4_RABIT 60.2 23.7 1935 1 MYH4_RABIT 60.2 29.9 1935 1 MYH7_HUWAN 60.2 20.9 1935 1 MYH7_HUWAN 60.2 20.0 1935</td> <td>Querry Querry 248 98.0 115 1 PTHY_HOWAN P01270 241 95.3 115 1 PTHY_MCPA 2041 241 95.3 115 1 PTHY_MCPA 20212 199 78.7 115 1 PTHY_RACPA P01269 194 76.7 115 1 PTHY_RACPA P01269 68.5 27.1 115 1 PTHY_RACPA P01269 68.5 27.1 119 1 PTHY_RACPA P01269 61.5 24.9 1937 1 WYHB_HUMAN P1353 61.5 24.9 1937 1 WYSS_RAPIT P02662 60.23.7 1934 1 WYSS_RAPIT P02663 60.23.7 1935 1 WYHA_RABIT P02664 60.23.7 1936 1 WYHA_RABIT P024466 58 22.9 1935 1 WYHA_RABIT P02448 58 22.9 1935 1 WYHA_RAM P1288 58 22.9 1935 1 WYHA_RAM <td< td=""><td>Score Match Length DB ID 248 98.0 115 1 PTHY_HUMAN 241 95.3 115 1 PTHY_HUMAN 241 95.3 115 1 PTHY_ACPA 242 115 1 PTHY_ACPA 243 115 1 PTHY_ACPA 244 98.0 115 1 PTHY_ACPA 245 115 1 PTHY_ACPA 246 5.3 115 1 PTHY_BOUTH 247 115 1 PTHY_BOUTH 248 27.1 119 1 PTHY_RAT 248 27.1 119 1 PTHY_RAT 248 27.1 119 1 PTHY_RAT 249 1937 1 MYHB_HUMAN 249 1935 1 MYHB_HUMAN 250 23.7 1084 1 MYSS_CYPCA 251 1 1936 1 MYHB_CHICK 252 1 1936 1 MYHB_CHICK 253 1 1 1084 1 MYSS_CYPCA 254 2 1935 1 MYHB_CHICK 255 2 1 1936 1 MYHB_CHICK 256 2 2 1 1935 1 MYHB_CHICK 257 1 1940 1 MYHB_CHICK 258 2 2 9 1935 1 MYHB_CHICK 259 1935 1 MYHB_CHICK 250 1935 1 MYHB_CHICK 250 1935 1 MYHB_CHICK 251 1936 1 MYHB_CHICK 252 1 1936 1 MYHB_CHICK 253 2 1936 1 MYHB_CHICK 254 2 1937 1 MYHB_CHICK 255 2 2 1937 1 MYHB_CHICK 256 2 2 1 1936 1 MYHB_CHICK 257 2 2 1 1936 1 MYHB_CHICK 257 2 2 1 1937 1 MYHB_CHICK 258 2 2 1937 1 MYHB_CHICK 259 1937 1 MYHB_CHICK 250 1937 1 MYHB_CHICK 250 2 2 1 1937 1 MYHB_CHICK 250 2 2 1 1937 1 MYHB_CHICK 250 2 2 1 1937 1 MYHB_CHICK 250 2 2 1937 1 MYHB_CHICK 250 2 2 1 1937 1 MYHB_CHICK 260 2 2 1 1937 1 MYHB_CHICK 270 2 2 1 1937 1 MYHB_CHICK</td><td>Score Match Length DB ID 248 98.0 115 1 PTHY_HOWAN 241 95.3 115 1 PTHY_ACRA 206 B1.4 115 1 PTHY_CANPA 194 76.7 115 1 PTHY_EACH 194 76.7 115 1 PTHY_EACH 68.5 27.1 119 1 PTHY_ENCT 68.5 27.1 119 1 PTHY_ENCT 69.2 24.9 1937 1 MYH8_HOWAN 60.2 23.7 1935 1 MYSS_RABIT 60 23.7 1935 1 MYSS_RABIT 60 23.7 1940 1 MYSS_RABIT 60 23.7 1940 1 MYH3_CHCK 58 22.9 1935 1 MYH4_RABIT 58 22.9 1935 1 MYH7_HOWAN 58 22.9 1935 1 MYH7_HOWAN 59 22.9 1935 1 MYH7_HOWAN 51 22.9 1935 1 MYH7_HOWAN 52 22.7 378 1 ULZS_HSV6G 52 22.7 378 1 ULZS_HSV6G 53 22.7 378 1 ULZS_HSV6G 54 22.7 378 1 ULZS_HSV6G 55 22.7 378 1 ULZS_HSV6G 55 22.7 378 1 ULZS_HSV6G 57 22.7 378 1 ULZS_HSV6G 58 22.9 1939 1 MYH7_HOWAN 69 22.7 555 1 ULZS_HSV6G 65 22.7 378 1 ULZS_HSV6G 65 22.7 378 1 ULZS_HSV6G 65 22.7 378 1 DYH4_HOWAN 69 97 623 4 60 23.7 1939 1 MYH4_HOWAN 60 97 623 4 60 22.7 378 1 ULZS_HSV6G 60 22.7 378 1 ULZS_HSV6G 60 22.7 378 1 DYH4_HOWAN 60 97 623 4 60 22.7 378 1 DYH4_HOWAN 60 97 623 4 60 22.7 378 1 DYH4_HOWAN 60 97 623 4 60 22.7 378 1 DYH4_HOWAN 60 97 623 4 60 22.7 378 1 DYH4_HOWAN 60 97 623 4 60 22.7 378 1 DYH4_HOWAN 60 97 623 4 60 22.7 378 1 DYH4_HOWAN 60 97 623 4</td><td>Querry Querry 248 98.0 115 1 PTHY_HOWAN P01270 241 95.3 115 1 PTHY_MCPA 204 15212 199 78.7 115 1 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27.1 119 1 PTHY_BNT 60.2 27.1 119 1 PTHY_RAT 60.2 23.7 1084 1 MYSS_RABIT 60.2 23.7 1084 1 MYSS_CYPCA 60.2 23.7 1938 1 MYHS_CHOCK 60.2 27 1938 1 MYHS_CHOCK 60.2 27 1938 1 MYHS_CHOCK 60.2 27 1940 1 MYHS_CHOCK 60.2 24 1940</td><td>Score Match Length DB ID 248 98.0 115 1 PTHY_HOWAN 241 95.3 115 1 PTHY_ACPA 240 98.0 115 1 PTHY_ACPA 241 95.3 115 1 PTHY_ACPA 242 115 1 PTHY_ACPA 243 115 1 PTHY_CANPA 194 76.7 115 1 PTHY_PIG 160 53.2 115 1 PTHY_PIG 68.5 27.1 119 1 PTHY_PIG 60.5 27.1 119 1 PTHY_CHOKAN 60.5 23.7 1937 1 MYH8_HOMAN 60.23.7 1935 1 MYH8_HOMAN 60.23.7 1940 1 MYH8_CHOKAN 60.23.7 1940 1 MYH3_CHICK 60.23.7 1940 1 MYH4_HOMAN 60.24.6 1940 1 MYH4_HOMAN 60.25.6 1940 1 MYH4_HOMAN 60.25.7 378 1 UIZS_HSV6U 60.22.7 378 1 UIZS_HSV6U 60.22.7 378 1 MYH4_HOMAN 60.22.7 378 1 MYH4_HOMAN 60.22.7 378 1 MYH4_HOMAN 60.23.7 1936 1 MYH4_HOMAN 60.23.7 1936 1 MYH4_HOMAN 60.23.7 1938 1</td><td>Score Match Length DB ID 248 98.0 115 1 PTHY_HOWAN 249 98.0 115 1 PTHY_ACRA 240 98.0 115 1 PTHY_ACRA 240 98.0 115 1 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Q02566 mus musculu P02563 rattus norv P13539 mesocricetu Q06700 acidaminoco Q041f5 pyrococcus O74092 pyrococcus O59255 schizosacch Q9h0b6 homo sapien P04461 oryctolagus P93331 lycopersico Q63259 rattus norv P75310 mycoplasma
MYH6_MOUSE MYH6_RAT MYH6_MEAU GCDM_ACIFE HARB_PYRAB HARB_PYRAB HARB_PYRAD TDG_SCHPO KLC2_HUMAN MYH7_RABIT VP41_LYCES PTPN_RAT
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ALIGNMENTS

RESULT 1 PTHY_HUMAN IDD PTHY_HUMAN DT 21-JU DT 21-JU DT 13-AU DT 13-AU DD 13-AU DD 13-AU DD 13-AU DD 13-AU DD 13-AU GN PTH. GN PTH. GO MAMMAN OC MAMMAN RE POLICIE RE RE SEQUES RE NOCICIE RE SEQUES RE MEDLINE RE MEDLI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
Rronenberg H.M.;
Mutation of the signal peptide-encoding region of the
preproparathyroid hormone gene in familial isolated
hypoparathyroidism.";
J. Ciln. Invest. 86:1084-1087(1990).
I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
I- DISEASE: Defects in PTH are a cause of familial isolated
hypoparathyroidism (FIH) [MIX:146200].
I- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRÜCTURE BY NMR OF 32-65.
MEDLINE-1199748. Pubmed-2069952;
MEDLINE-1199748.
MIDLECKMAND T., Wray V., Schomburg D., Wingender E., Mayer Innvestigation of the solution structure of the human parathyroid bromone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and molecular dynamics calculations.";
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*Synthesis of sequence 1-34 of human parathyroid hormone.";
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Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.
Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31ochem. Blophys. Res. Commun. 267:213-220(2000)
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MEDLINE-20090619; PubMed-10623601;
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Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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GO:0007267; P:cell-cell signaling; Tas.
GO:0007186; P:G-protein coupled receptor protein signa
GO:0008628; P:induction of apoptosis by hormones; Tas.
GO:0001501; P:skeletal development; Tas.
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Pred. No. 1.9e-23;
1; Mismatches 0; Indels
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/FIId-VAR_006047.
N -> D (IN REF. 5).
                                                                                                                                                                                                                                     generating peptide activity; TAS
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12861 MW; 849015736A6E5597 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                   PARATHYROID HORMONE.
                                                                                                                                                                                                                                                                                                                                                                   Signal; Disease mutation; 3D-structure.
email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                  InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
                                                                                                                                                                                                                                                                                                                                    ProDom; PD010687; Pthyrhorm_sub; l.
                                                                                                                                                                                                                                                                                                                                                        PS00335; PARATHYROID; 1
                                                                                                                                                                                                                                                                                                                         PF01279; Parathyrold; 1
                    EMBL; J00301; AAA60215.1; -. EMBL; V00597; CAA23843.1; -. EMBL; A29146; CAA01956.1; -.
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98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            107
                                                                                                                                                                                           1FVY; 31-DEC-02.
                                                             1HPH; 10-JUL-95
1HTH; 15-OCT-97
                                                                                   12WA; 12-MAR-97
                                                                                             12-MAR-97
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64
115 AA;
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                                                                                                                                                                   PDB; IET1; 06
PDB; IET2; 06
PDB; IFVY; 31
Genew; HGNC:9
                                                     PIR; A19339;
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Best Local Simi
Matches 50;
                                                                                                                   1ZWE;
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09XT35;
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Hormone;
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HELIX
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JC4202.
                                      HSSP; P01268; 12WC
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                                                                                                                                                  Hormone; Signal
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P01268;
21-JUL-1986 (
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28-FEB-2003 (
Parathyroid H
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                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseefsb-sib.ch).
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Malalvijitnond S., Takenaka O.:
"Nucleotide sequences of parathyroid gene in five species of macaque
of Thailand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                           J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Parathyroid;
MEDLINE-95369696; PubMed-7642102;
Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
DeWille J.W., Capen C.C.;
"Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone.";
Gene 160:241-243(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BONE AND PREVENTING THEIR RENAL EXCRETION.
SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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PARATHYROID HORMONE.

8C2500EF248E5597 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.3%; Score 241; DB 1;
92.2%; Pred. No. 1.3e-22;
cive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AA
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InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
                                                                                                                                                                                                                                                                                                              Pfam: PF01279; Parathyroid; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 12890 MW;
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115 AA;
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P52212;
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Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr., Cohn D.V.,
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                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at the 5' terminus of the sense strand of bovine parathyroid hormone CDNR.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-83105964; PubMed-6185374;
Weaver C.A., Gordon D.F., Kemper B.;
"Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
Mol. Cell. Endocrinol. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84262483; Pubmed-6086460; Weaver C.A., Kemper B.; Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.; "Isolation and complete nuclectide sequence of the gene for bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                              51
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0
                                                                                                                                                                                                                                                                                              1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ
                                                                                                                                                                                                          81.4%; Score 206; DB 1; Length 115; 82.4%; Pred. No. 2.5e-18; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-82037785; PubMed-6170060;
Weaver C.A., Gordon D.F., Kemper B.;
"Introduction by molecular cloning of artifactual inverted
                                                                                                                       25 BY SIMILARITY.
31 BY SIMILARITY.
115 PARATHYOLD HORMONE.
12957 MW; PC38F77F1C8CFE56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preproparathyroid hormone.";
Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                     115 AA
InterPro: IPR001415; Parathyrd_hrm.
InterPro: IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyro14; 1.
SMART; SM00087; Pthyrhorm_sub; 1.
SMART; SW00087; Pthy. 1.
PROSITE; PS00335; PARATHYROID; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 01, Created)
(Rel. 01, Last sequ
(Rel. 41, Last anno
                                                                                                                                                                                                                          Best Local Similarity 82.4 Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taurus (Bovine).
                                                                                                                                                                         115 AA;
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115 AA.

PRT;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
    65 FVALGASIAYRDGSSQRPRKKEDNVLVESHQKSLGEADKADVDVLIKAKPQ 115
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDI.NE-87316938; PubMed-3628009;
MEDI.NE-87316938; O., Widera G., Mayer H...
"Nucleotide sequence of a full-length cDNA clone encoding preproparathyrold hormone from plg and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Parathyrold hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                           scrofa (Pig).
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Matches
                                                             RESULT 5
PTHY_PIG
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute, There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                         XYNTHESIS OF 32-65.
MEDLINE-71091588; PubMed-4322265;
Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
Deftos J.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
"Synthesis of a biologically active N-terminal tetratriacontapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blochem. Blophys. Res. Commun. 267:213-220(2000).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-20090619; Pubmed-10623601;
Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
Solution structures of human parathyroid hormone fragments
hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
                                                                      MEDLINE-71076162; PubMed-5531031;
Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
Aurbach G.D., Ports J. Jr., Jr.,
"The amino acid sequence of bovine parathyroid hormone I.";
Hoppe-Seyler's 2. Physiol. Chem. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 115;
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12980 MW; 2ED246B348B80710 CRC64;
                                                                                                                                                                                                                                                       "Bovine parathyroid hormone: amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.7%; Score 199; DB 1; Lx 80.4%; Pred. No. 1.8e-17; Lve 4; Mismatches 6;
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lormone.";
roc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
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InterPro; IPR003625; Pchyrhorm_sub,
Pfam; PF01279; Parathyroid; IP
ProDom; PD010687; Pthyrhorm_sub; I.
                                                                                                                                                                                       SEQUENCE OF 32-115.
MEDLINE-71063634; PubMed-5275384;
Brewer H.B. Jr., Ronan R.;
"Bovine parathyroid hormone: aming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00335; PARATHYROID; 1. Hormone; Signal; 3D-structure.
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EMBL; K01938; AAA30749.1; --
EMBL; M25082; AAA30748.1; --
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                                                   SEQUENCE OF 32-115.
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Best Local Similarity
Matches 41; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                  SEQUENCE OF 32-115.

MEDILINE-7425317; PubMed-4840833;

Squer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,

Potts J.T. Jr.,

"The amino acid sequence of porcine parathyroid hormone.";

"The amino acid sequence of porcine parathyroid hormone.";

Blochemistry 13:1994-1999(1974).

-!- FUNCTION: PTH ELENATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

BONE AND PREVENTING THEIR RENAL EXCRETION.

-!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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SEQUENCE OF 26-115.
MEDLINE=76018954; PubMed=1164500;
Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
"Porcine proparathyroid hormone. Identification, biosynthesis, and partial amino acid sequence.";
Biochemistry 14:3631-3635(1975).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 76.7%; Score 194; DB 1; Length 11 Local Similarity 78.4%; Pred. No. 7.3e-17; es 40; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9FE8BCDE614BAC16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARATHYROID HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001415; Parathyrd_hrm.
InterPro: IPR003625; Pthyrhorm_sub.
Pfam: PF01279; Parathyrodd; 1.
ProDom: PD010687; Pthyrhorm_sub; 1.
SWART; SM00087; PTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
31
115
12852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X05722; CAA29193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01270; 1BWX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B26806: PTPG
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1 FVALGAPIAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSO 51

Conservative

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s in no way
for commercial
                                                                                                                                  PTH.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Bukaryota; Butherla; Rodentla; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endocrinology 136:5600-5607(1995).
-!- FUNCTION: PTH ELEYATES CALCIUM LEYEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-!- TISSUE SPECIFICITY: HYPOTHALAWUS AND PARATHYROID GLAND.
-!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmelzer H.J., Gross G., Mayer H.; "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.";
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDIINE-6413546; Pubmed-6321505;
Helnich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
"Gene encoding parathyrold hormone. Nucleotide sequence of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 32-115 FROM N.A. STRAIN-STRAIN, Liver, and Parathyroid; STRAIN-SPRGYPOUTO; TISSUE-Brain, Liver, and Parathyroid; MEDLINE-9679910; PubMed-7314; Nutley M.T., Parini S.A., Harvey S.; Sequence analysis of hypothalamic parathyroid hormone messenger
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIINE-87316938; PubMed-3628009;
Schmelzer H.-J., Gross G., Widera G., Mayer H.;
Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
                                            P04089; Q63473;
01-NOV-1986 (Rel. 03, Created)
10-NOV-1986 (Rel. 03, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARATHYROID HORMONE. C -> Y (IN REF. 3).
                                 115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; K01268; AAA41979.1; -.
EMBL; X05721; CAA29192.1; -.
EMBL; M54875; AAA57156.1; -.
EMBL; S80127; -; NOT_ANNOTATED_CDS.
PIR; A05091; A05091.
HSSP; P01270; 12WB.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001415; Phyrhorm_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adv. Gene Technol. 21:228-229(1984).
                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 259:3320-3329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01279; Parathyrold; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 10-115 FROM N.A.
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00087; PTH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSUE-Parathyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribonucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                        hormone.
                               PTHY_RAT
P04089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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                   PTHY_RAT
RESULT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDINE-99219100; Pubmed-2710135; MEDLINE-99219100; Pubmed-2710135; Russell J., Sherwood L.M.; "Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone mRNA and the deduced sequence of the
                                                                                                                                                                                                                                                                     1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Pred. No. 0.16;
                                                                                                                                    Score 160; DB 1; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
Kronenberg H.M.;
  A -> T (IN REF. 3).
V -> I (IN REF. 3).
V -> G (IN REF. 3).
7B434CFCA528B230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 31 PARATHYROID HORMONE.
32 119 PARATHYROID HORMONE.
119 AA; 13943 MW; B309D8E772997F6E CRC64;
                                                                                                                                                                                        11;
                                                                                                                                                          le-12;
                                                                                                        62.7%; Scort No. 15 - 62.7%; Pred; No. 15 - 62.7%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Parathyroid hormone precursor (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A34937; A34937.
HSSP; P01270; 1HPY.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Endocrinol. 3:325-331(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89284968; PubMed-3251402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
  23 A
33 V
62 V
12722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last seq 15-JUL-1998 (Rel. 36, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.1%;
38.9%;
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                                                                                                                                                                                     32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
  23
33
62
115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                        PTHY_CHICK
P15743;
CONFLICT
CONFLICT
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SEQUENCE
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SEQUENCE
                                                                                                                                    Query Match
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Matches
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  SFFF
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-!- SIMILARITY: Contains 1 10 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification of three developmentally controlled isoforms of human
       Gaps
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                                                           Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S., Stedman H.H., Rubinstein N.A.;
                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular genetic characterization of a developmentally regulated numan perinatal myosin heavy chain."; Cell Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90323631; PubMed-2373371;
Karsch-Mizrachi I., Feghall R., Shows T.B. Jr., Leinwand L.A.;
"Generation of a full-length human perimatal myosin heavy-chain-
                                                                                                                                                                                     P13535; Q14910;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myosin heavy chain, skeletal muscle, perinatal (MyHC-perinatal).
                                   9 APRDAGSQRPRKKEDNVLVE-----SHEKSLGEANKADVNVLTKAK
       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERISTIC FOR ALPHA-HELLCAL COILED COILS.
PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN APPASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBFRAGMENT (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Characterization of a human perinatal myosin heavy-chain
     Indels
     14;
                                                                                                                                                                         PRT; 1937 AA.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ur. J. Blochem. 230:1001-1006(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 860-1937 FROM N.A. WEDLINE-89234168; Pubmed=2715179; Peghall R., Leinwand L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Skeletal muscle;
MEDLINE-95324556; PubMed-7601129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nyosin heavy chains.";
Sur. J. Biochem. 189:55-65(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDLINE-90235862; PubMed-1691980;
 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF 502-1937 FROM N.A.
 Conservative
                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        INSUE-Skeletal muscle;
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                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding cDNA
21;
                                                                                                                                                                   MYH8_HUMAN
P13535; 014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ranscript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD000355; myosin_head; 1.
SWART; SW0015; IQ; 1.
SWART; SW00242; MSC5: 1.
PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Colled coil; Thick fillament; Actin-binding;
ATP-binding; Methylation; Alkylation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYLATION (TRI-) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63; DB 1; Length 1937;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1378 KY -> NT (IN REF. 3).
1505 EN -> AH (IN REF. 1 AND 4).
1847 E -> D (IN REF. 2).
1914 D -> H (IN REF. 2).
1222762 MW; A3EEZD151792E9E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                        F:structural constituent of muscle; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND 4).
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COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 32, Created)
(Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 16;
9; Mismatches
                                                                                                                                                                                                                                                                                      Genew; HGNC:7578; MYH8.

MIM; 160741; -..
GO; GO:0005859; C:muscle myosin; TAS.
GO; GO:0008307; F:structural constituen
InterPro; IPR001609; IQ_region.
InterPro; IPR001609; Myosin_head.
InterPro; IPR004099; Myosin_head.
InterPro; IPR004099; Myosin_head.
InterPro; IPR004099; Myosin_tail.
Pfam; PF00612; IQ; I.
                                                                                                                                                                                 EMBL; Z38133; Cencer; EMBL; X51592; CAA35941.1; --
EMBL; AF067143; AAC21557.1; --
PIR; I38055; I38055. HSSP; P13538; ZMIS.
Genew; HGNC:7578; MIH8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                    EMBL; M36769; AAC17185.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 24.9%;
l Similarity 42.4%;
14; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calmodulin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1847
1914
1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
YEO5_HAEIN
ID YEO5_HAEIN
AC P44180;
DT 01-NOV-1995 (
DT 01-NOV-1995 (
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Best Local S
Matches 14
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                      FIRATINE KWAZEN ATCC 51907;

MEDIATRE-95350630; PubMed-7542800;

Fleischmann R.D., Addams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.T., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.3%; Score 61.5; DB 1; Length 366; 35.6%; Pred. No. 3.9; ive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 PLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGH, HI1405; --
TIGH, HI1405; --
HYPOTHETICH protein; Complete protecome.

FROUENCE 366 AA; 40122 MW; 68040800B631AECO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus (type 6 / strain 229) (HHV6).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein HI1405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95074921; PubMed-7983761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32820; AAC23055.1; -. PIR; A64028; A64028.
                                                                                                                                                                                                                                                                                                                                                    Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                              Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virion protein U50.
U50 OR KAIIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 16; Conserv
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=36351
                                                                                             NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UL25_HSV62
P52537;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i-SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-i-SUBCELLULAR LOCATION: THICK filaments of the myofibrils.
-i-DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 20-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
-I-MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND I HEAVY MEROMYOSIN (HAM). IT CAN LAPER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND I ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 409-1084 FROM N.A.

MEDLINE-87304245; Pubmed-3305014;

MEDLINE-87304245; Pubmed-3305014;

"Characterization of CDNA coding for the complete light meromyosin portion of a rabbit fast skeletal muscle myosin heavy chain.";

PURTION: MUSCLE CONFRACTION.

-1 - FUNCTION: MUSCLE CONFRACTION.

-1 - SUBUNIT: MUSCLE MOSSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Myosin heavy chain, skeletal muscle (Fragments).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capony J.-P., Elzinga M.; "The amino acid sequence of A 34,000 dalton fragment from S-2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lu R.C., Wong A.; "The amino acid sequence and stability predictions of the hinge
                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
                                                                                                                                                                                                                                         Length 555;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                      68B86590DC4CD2BC CRC64;
                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                  16 QRPRKKEDNVLVESHEKSLGEA----NKADVNVLTKAKSQ
                                                                                                                                                                                                                                       Score 60.5; DB 1;
Pred. No. 8.3;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1084 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 260:3456-3461(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-85131142; PubMed-3972832;
Lu R.C., Wong A.;
                                                                                                                       EMBL; AF157706; AAB06348.1; -. PIR; T44010; T44010. InterPro; IPR002493; UL25. Pfam; PF01499; UL25; 1. SEQUENCE 555 AA; 63830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. 33:148A-148A(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region in myosin subfragment
                                                                                                                                                                                                                                       23.9%;
llarity 42.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE OF 259-428
                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONSERVED
                                                                                                                                                                                                                                                                                                                                                                                                                                               MYSS_RABIT
P02562;
                                                                                                                                                                                                                                         Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MYSS_RABIT
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Myosin heavy chain, fast skeletal muscle.
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygil; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skeletal
                                                                                                                                                                                                                           Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1387-1528 FROM N.A.
MEDLINE-95194396; PubMed-7887920;
Watabe S., Imal J., Nakaya M., Hirayama Y., Okamoto Y., Masaki H.,
Watabe S., Imal J., Aoki T.;
"Temperature acclimation induces light meromyosin isoforms with
different primary structures in carp fast skeletal muscle.";
Blochem. Blophys. Res. Commun. 208:118-125(1995).
-!- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=FRAST muscle;
MEDLINE-97352533; PubMed-9208928;
Hirayama Y., Watabe S.;
"Structural differences in the crossbridge head of temperature-associated myosin subfragment-1 isoforms from carp fast skeletal
                                                                                                                                                                                                                                                                                                                                                                     RODLIKE TAIL (S2 AND LMM DOMAINS). COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97176447; Pubmed-9023993; Imal J., Hirayama Y., Kakuchi K., Kakinuma M., Watabe S.; Chual J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.; Chual Cloning of myosin heavy chain isoforms from carp fast smuscle and their gene expression associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1084;
                                                                                                                                                                                                                                                                                                                ALPHA-HELICAL TAILPIECE (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E -> D.
S -> G.
K -> R.
MW; 229CFD69A6ElF7F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60; DB 1;
Pred. No. 20;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1935 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             · ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Blochem. 246:380-387(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 981-1935 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ciimation.";
Exp. Biol. 200:27-34(1997).
                                                                                                            EMBL; X05958; CAA29391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 42.4%; es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AA;
                                                                                                                                                                    A05280; A05280
S00084; S00084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'ISSUE-Fast muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYSS_CYPCA
Q90339;
                                                                                                                                                                                                                                                                                                             DOMAIN
NON_CONS
DOMAIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
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Matches
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                                                                                                                                                                                                       PIR;
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SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
FIM. TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATRASE ACTIVITY.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT WEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 10 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
MW. 9A1244867D63C83B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60, DB 1; Length 1935;
Pred. No. 38;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Methylation; Alkylation; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HINGE. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
y chain, skeletal muscle, juvenile
cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1938 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ffam; PF00612; 10; 1.
Pfam; PF00612; 10; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF01776; Myosin_n; 1.
PRINTS; PR00193; MYOSINHBAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                            EMBL; D89992; BAA22069.1; ... EMBL; D50476; BAA09069.1; -.. EMBL; D43700; BAA07802.1; -.. PIR; I50496; I50496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 23.7%;
Local Similarity 42.4%;
es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, La 28-FEB-2003 (Rel. 41, Lu Myosin heavy chain, ske. Oryctolagus cuniculus (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          761
129
129
696
706
1935 AA;
                                                                                                                                                                   SUBFRAGMENT (52)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYH4_RABIT
Q28641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
SEQUENCE
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
MYH4_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                          Transpared to the Emphasis of Standards of Augusting March 1970 of March
                                                                                                                                              SEGUENCE FROM N.A.
STRAIN-New Zealand white; TISSUE-Skeletal muscle;
Macda K., Hostinova E., Roesch-Kleinkauf A., Schuster H., Gasperik J.,
Wittinghofer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1938 | COLLED COLL (POTENTIAL). |
| 1938 | ATP (POTENTIAL). |
| 1940 | ACTIN-BINDING (BY SIMILARITY). |
| 1951 | ACTIN-BINDING (BY SIMILARITY). |
| 1952 | ACTIN-BINDING (BY SIMILARITY). |
| 1953 | ACTIN-BINDING (BY SIMILARITY). |
| 1954 | ACTIN-BINDING (BY SIMILARITY). |
| 1955 | ACTIN-BINDING (TRI-) (BY SIMILARITY). |
| 1956 | ALKYLATION (TRI-) (BY SIMILARITY). |
| 1957 | ALKYLATION (SH-1) (BY SIMILARITY). |
| 1958 | ALKYLATION (SH-1) (BY SIMILARITY). |
| 1959 | ALKYLATION (SH-2) (BY SIMILARITY). |
| 1950 | ALKYLATION (SH-2) (BY SIMILARITY). |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation;
Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus,
NCBI_TaxID-9986,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 myosin-like globular head domain.
SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001048; IQ_region.
InterPro; IPR001009; Myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR004009; Myosin_N.
InterPro; IPR004009; Myosin_N.
InterPro; IPR004009; Myosin_tail.
InterPro; IPR00103; Myosin_tail.
IPRINTS; PR00193; MYOSINHEAVY;
IPROP; IPR000355; Myosin_head; ISMART; SM00015; IQ; I.
SMART; SM00015; IQ; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U32574; AAA74199.1; -. PIR; A59293; A59293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00242; MYSc; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 191
1942 19
1942 19
658 66
760 77
35 13
130 13
552 552
756 69
708 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12. 3. BIOL. Chem. 258:5196-5205(1983).
12. 3. BIOL. Chem. 258:5196-5205(1983).
13. SIOL. Chem. 258:5196-5205(1983).
14. SUBUNIT: MUSCLE MODIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).
15. STEGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
16. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
17. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
18. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
19. CYCLES OF A 28 RESIDIOE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.
19. CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLED.
19. PTW. TWO CYSTEINE RESIDIES IN THE 51 DOMAIN ARE SELECTIVELY ALKYLAND AND ARE REDUIRED FOR MYOSIN APPASE ACTIVITY.
19. CHARACTERISTIC CHAM) AND ARE NEGULIED.
20. HISCELLANDOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LAFER BE SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1502-1940 FROM N.A.
MEDIALTHE-BIBLIA4; Pubmeda-6833396;
Kavinsky C.J., Umeda P.K., Sinha A.M., Elzinga M., Tong S.W., Zak R.,
Jakovcic S., Rabinowitz M.;
"Clonde mana sequences for two types of embryonic myosin heavy chains
from chick skeletal muscle. I. DNA and derived amino acid sequence of
light meromyosin.";
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                  MEDLINE-87194881; PubMed-3571266;
Molina M.I., Kropp K.E., Gulick J., Robbins J.;
"The sequence of an embryonic myosin heavy chain gene and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFRAGMENT (S2).
-1- SIMILARITY: Contains 1 myosin-like globular head domain.
-1- SIMILARITY: Contains 1 IQ domain.
                                        21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myozin heavy chain, fast skeletal muscle, embryonic.
  PRT; 1940 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   of its corresponding cDNA.";
J. Biol. Chem. 262:6478-6488(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan; PF02736; Myosin_N; 1.
Pfan; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'fam; PF00063; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V00430; CAA23712.1; -. EMBL; J02714; AAA48972.1; -. PIR; A29320; A29320.
    STANDARD;
                                                                                                                                                     Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fam; PF00612; IQ; 2.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                        NCBI_TaxID-9031;
MYH3_CHICK
P02565;
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ij

Gaps

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Length 1938;

Score 60; DB 1; Pred. No. 38;

23.78;

8; Mismatches

14; Conservative

Best Loc Matches

Local Similarity

Query Match

Gaps

13;

Length 527; 17; Indels

DB 1;

Score 58.5; DB Pred. No. 14; 7; Mismatches

367 POLY-ASP. 527 59258 MW; ABEF4B10C086D638 CRC64;

us-09-928-048a-5.rsp

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9 APRDAGSORPRKKEDNV-----LVESHEKS-----LGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                           Search completed: October 9, 2003, 08:11:22 Job time : 10.8955 secs
                                                                                   Query Match 23.1%;
Best Local Similarity 33.9%;
Matches 19; Conservative
    360
527
527 AA;
    DOMAIN
NON_TER
SEQUENCE
      FT
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                                                                                                                                                                                                        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obsawa K., Imal Y., Ito D., Kohsaka S.;
"Molecular cloning and characterization of annexin V-binding proteins with highly hydrophile peptide structure.";
"Molecular cloning and characterization of annexin V-binding proteins with highly hydrophile peptide structure.";
-1. FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL RECULATOR. MODIFIES GENE EXPRESSION BY AFFECTING CHROMATIN.
-1. SUBUNIT: PROBABLY BINDS ELECTING AND PHOSPHATIDYLCHOLINE, PHOSPHATIDYLSERINE-DEPENBENT MANNER.
-1. SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH PERICENTROMERIC HETEROCHROMATIN DURING INTERPHASE AND MITOSIS, PROBABLY BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nattus norvegicus (Rat).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                  PROSITE; PSS0096; IQ; 1.
Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding;
Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-2003 (Rel. 41, Created)
18-FEB-2003 (Rel. 41, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Franscriptional regulator ATRX (X-linked nuclear protein) (pABP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                    ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (FIL-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTING WITH HPI (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                            G -> D,
T -> A (IN REF. 2).
ERA -> GRT (IN REF. 2).
IW; C34833D75B04DFF2 CRC64;
                                                                                                                                            IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA repair; Nuclear protein; DNA-binding; Helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21. KEDNVLVESHEKSLG -- EANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 38;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION,
                                                                                                                                                                                                                                                                                                                                                                                                              Score 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Wistar; TISSUE-Embryonic brain; dEDLINE-96301899; PubMed-8667030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                              1915 EKA
: 222816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          23.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D64059; BAA10936.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                1913 19.
1940 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CBI_TaxID-10116;
                                                                                               Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ragment).
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CONFLICT
SEQUENCE
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                                                                                                                                                                                TP_BIND
                                                                                                                                                               DOMAIN
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paracirrhit

gallus gall caenorhabdi

homo saplen

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Total number Minimum DB : Maximum DB :

Database

Searched:

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

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091bd7 seriola dum
09tv63 aus scrofa
09tv61 aus scrofa
09be41 bos taurus
                                                                                                                                                                                                                                                                           017490 caenorhabdi
052585 pseudomonas
09tyv5 caenorhabdi
005090 nocardioide
08ny08 staphylococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q28829 oryctolagus
Q92679 homo sapien
Q9vrp4 drosophila
Q91ys4 mus musculu
                                                                                                                                                                           Q8ay28 gallus gall
Q9dgm4 gallus gall
Q8jg72 gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9m344 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               094gus oryza sativ
                                       Q8mjvl equus cabal
Q8mjv0 equus cabal
Q9be40 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                          09dgm5
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Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
"Molecular cloning of feline preproparathyroid hormone.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF309967; AAG30545.1;
HSSP; P01268; 12WC.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
PARATHYROID HORMONE.
80CD557CC6AlA47E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Preproparathyroid hormone precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 205; DB 6; I
Pred. No. 3.6e-18;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                           Q8AY28
Q9DGM4
Q9DGM5
Q9DGM5
Q17490
Q17490
Q52585
Q09TYW5
Q8NY08
Q8NY08
Q90YE6
Q9TV62
Q8MJV1
Q9BE40
Q9IBD7
Q9TV63
Q9TV61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             094GU9
026829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01279; Parathyrold; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SWART; SW00087; PTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 096157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 25 P
32 115
115 AA; 12921 MW;
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Similarity 80.4%;
41; Conservative
                                                                                                                                                                                                                                                                                               909
                                                         NCBI_TaxID-9685;
  Query Match
Best Local S1
Matches 41;
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GL67
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Q9GL67
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Q98tq5 notothenia
P87344 theragra ch
O93498 theragra ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       098tq6 notothenia
099wc5 staphylococ
090338 cyptinus ca
09dd5 pennahla ar
0910c5 gallus gall
04252 cyptinus ca
090337 cyptinus ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            092016 mus musculu
09azw5 bacterlopha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9cfn5 lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9g167 felis silve
Q9n1v0 equus cabal
                                                                                                                          2003, 08:08:56; Search time 45.6716 Seconds (without alignments) 288.159 Million cell updates/sec
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                                                                                                                                                                                                                                                      51
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                                                                                                                                                                                                                             253
1 FVALGAPLAPRDAGSQRPRK......KSLGEANKADVNVLTKAKSQ
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                         - protein search, using sw model
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Q9Z0L6
Q9AZWS
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093498
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                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_mammal:*
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score greater than or equal to
and is derived by analysis of
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sp_vertebrate:
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sp_bacteriap:*
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sp_bacteria:*
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Match 1
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63.5

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115 AA; 12825 MW; DA43FABBCB4E2FD9 CRC64;
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                                                 Query Match
Best Local Similarity
Matches '31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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01-JUN-2001
01-DEC-2001
SEQUENCE
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Q9AZWS
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SEQUENCE FROM N.A.
MEDLINE-20082971; PubMed-10613847;
Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.;
"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:129-1249(1999).
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID-9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN*129/Sv;
Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.
"Cloning of the murine gene encoding parathyroid hormone: genomic organization and nucleotide sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIALGAPIFERDGGSQRPRKKEDNVLIESHQXSLGEADKADVDVLSKTKSO 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 203; DB 6; Length 86
Pred. No. 4.7e-18;
7; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA; 9805 MW; 253184EA681A2022 CRC64;
                                                                                                                                                                                        Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Parathyroid hormone precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL, PARATHYROID HORMONE.
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                                                                                                                                          (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last seq
(TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01270; 1HPY.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
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InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
                                                                                        PRT;
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PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                          01-007-2000 (TrEMBLrel. 15, Cre 01-007-2000 (TrEMBLrel. 15, Las 01-JUN-2002 (TrEMBLrel. 21, Las Parathyrold hormone (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01279; Parathyroid; 1
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76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 76.5 tes 39; Conservative
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    Equus caballus (Horse).
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Q920L6;
                                                                                 Q9N1V0
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              RESULT 2
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MEDLINE-21235186; PubMed-11337471; MEDLINE-21235186; PubMed-11337471; MEDLINE-21235186; PubMed-11337471; MEDLINE-21235186; PubMed-11337471; Medisenbach J., Ehrlich S.D., Sorokin A.; The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis ILI403."; Genome Res. 11:731-753(2001). EMBL; AE006373; AAK05530.1; -.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria: Firmicutes: Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.; "Analysis of six prophages in Lactococcus lactis ILI403: different genetic structure of temperate and virulent phage populations."; Nucleic Acids Res. 29:644-651(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=151536;
                                                                                                                      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF322669; AR08289.1; - SEQUENCE 283 AA; 31164 MW; DF4094313735E02A CRC64;
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     Length 115;
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01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Prophage pl3 protein 59
Pl359 OR LL1432.
                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 158, DB 11;
Pred. No. 3.1e-12;
9; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 16;
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-21113149; Pubmed-11160885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.7%;
62.5%;
60.8%;
                                                 Conservative
                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 1 (TrEMBLrel. 1 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
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Gaps

5

Length 975;

Matches

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Eukaryota, Metažoa, Chordata, Čraniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Paracanthopterygii, Gadiformes, Gadidae, Theragra,
NCBI_raxID-48550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin heavy chain (Fragment).
Theragra chalcogramma (Alaska pollock).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUB-Fast muscle;
Togashi M., Hirayama Y., Kakinuma M., Watabe S., Ojima T.,
"CDNA cloning of Alaska polack fast skeletal muscle myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1 119 AA; 128626 NW; B8C5FECAE6F5B954 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL. AB000214; BAA19070.1; -- HSSP; 2NTS. LINESPIN. 2NTS.
                                                                                                                                           NON_TER 1 1
SEQUENCE .975 AA; .112313 MW; 2F7AD46A3419537F CRC64;
         sequences from Antarctic and tropical fish.";
slochem. Physiol. 127:575-588(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63; DB 13;
Pred. No. 40;
7; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                   Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ
                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin heavy chain (Fragment).
Theragra chalcogramma (Alaska pollock).
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                      HSSP; P03437; 1HTM.
InterPro; IPR002528; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PP01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002928; Myosin_tail.
Interpro; IPR000533; Tropomyosin.
Pfam: PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                       Comp. Blochem. Physiol. 127:575
EMBL; AJ243768; CAC27777.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%;
ilarity 45.5%;
conservative 7
                                                                                                                                                                                          Query Match
Best Local Similarity 45.59
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR000533;
Pfam; PF01576; Mvosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-48550;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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       coding
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                                                                                                                                                                                                                                                                                                                                                                                    P87344
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Matches
                                                                                                                                                                                                                                                                                                                                                     RESULT 8
P87344
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       FT ROCK CALL
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                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N., Kreis M., Kavanagh T., Entlan K.D., Rieger M., James R., Puldgdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A., Jones J., Palme K., Ansorge W., Delseny M., Bancroft I., Mewes H.W., Schueller C., Chalwatzis N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Notothenioidei; Notothenildae; Notothenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jamvry L., Ennion S., Ettelale C., Goldspink G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.1%; Score 63.5; DB 10; Length 487; 30.2%; Pred. No. 14;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 297336; CAB10227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 APRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487 AA; 54380 MW; 77D21D39D2FB4F20 CRC64;
                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
STE20-like kinase homolog (Kinase like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              098105;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Myosin heavy chain (Fragment).
                                                  15 SQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKS 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   975 AA.
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, ALIG1539, CAB78490.1;
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Notothenia coriiceps (black rockcod).
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan, PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMRT; SM00220; S_TKC; 1.
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
ses 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYOHC-A3 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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A PACACA CONTRACTOR OF THE STANDAR O

Best Loc Matches

RESULT 7 **098T05**

RAPPACOCOCOS REPARA

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Nishita K.; heavy

Length 1119;

Gaps

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SPECIES-S.aureus (strain MuSO), and S.aureus (strain N315);
MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cul L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatau K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyprinus carpio (Common carp).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes;
Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 AGGVSVAPAGKSSKKPARGIQKSKNAFSMQQIAKVLDKANKADIKLL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALGAPLAPRDAGSQRP----RKKEDNVLVESHEKSLGEANKADVNVL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 565;
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria: Firmicutes: Bacillales: Staphylococcus.
NCBL_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565 AA; 63471 MW; F29A7F07095F02AA CRC64;
                                                                                                                                                                                                                                                                                    on-mar-2003 (TremBirel. 17, Last sequence update)
DNA polymerase III gamma and tau subunits.
DNAX OR SAV0478 OR SA0436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
          6
                                                                                        ; Score 61; DB 16;
; Pred. No. 33;
11; Mismatches 17
                                                             21
                                                                                                                                                                                                                                      565 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1092 AA.
          Mismatches
                                                        21 KEDNVLVESHEKSLG -- EANKADVNVLTKAKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS00214; FABP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLPPROTEASEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.18;
31.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin heavy chain (Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP003359; BAB56640.1;
EMBL; AP003130; BAB41666.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lancet 357:1225-1240(2001)
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00004; AAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Local 15; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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        15;
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        Matches
                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          099WC5
                                                                                                                                                                                                                                                                                      DDT READ BY SEW 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                     Kawashima N., Inoue A., Amauchi A., Togashi M., Watabe S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Notothenia corilceps (black rockcod).

Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota: Neoperygii, Taleostai; Buteleostai; Neoteleostai;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Notothenioidel; Nototheniidae; Notothenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sauvry L., Ennion S., Ettelaie C., Goldspink G.,
Characterisation of red and white muscle myosin heavy chain gene
coding sequences from Antarctic and tropical fish.";
Comp. Blochem. Physiol. 127:575-588(2000).
                                                                             Meromyosin. Region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 1287; 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1287 AA; 146467 MW; BAD93CB005D6A7CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50096; IQ; 1.
SEQUENCE 1929 AA; 221167 MW; 20A78CBA19DE851B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                   "Determination of Primary Structure of Heavy Meromy Walleye Pollack Myosin Heavy Chain by cDNA Cloning. Fisheries Sci. 0:0-0(1998).
EMBL, AB017819; BAA33452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 KEDNVLVESHEKSLG.-EANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63; DB 1
Pred. No. 47;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1929 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPRO00048; IQ_region.
IPRO01609; myosin_head.
IPRO04009; Myosin_N.
IPR002928; Myosin_tail.
                                                                                                                                                                                   myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                       PF01576; Myosin_tail; 1.
5; PR00193; MYOSINHEAVY.
1; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                 myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.9%;
45,5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98TQ6;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                    PF02736; Myosin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF02736; Myosin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1
TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SMOLL | 10; 10; 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00015; IQ; 1
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                    fam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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098TQ6

RESULT 10 Q98TQ6 ID Q98TQ

nterPro nterPro

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Query Match Best Local S Matches 15

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SEQUENCE

PRINTS;

fam; Pfam: Gaps

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"Characterization and expression pattern of atrial myosin heavy chain gene in developing orlick.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB004801; BAB47399.1; -
InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_N.
InterPro; IPR001609; myosin_N.
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oana S., Machida S., Furutani Y., Hiratsuka E., Momma K., Takao A.,
Matsuoka R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Fast muscle;
MEDLINE-97352533; PubMed-9208928;
Hirayama Y., Watabe S.;
Hirayama Y., Watabe S.;
"Structural differences in the crossbridge head of temperature-associated myosin subfragment-1 isoforms from carp fast skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221802 MW; EB57D688E03397D2 CRC64;
                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 23, Last annotation update)
Chick artial myosin heavy chain.
Gallus gailus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.8e+02;
7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | :| |||:::| :| :| || || || || || 989 KEKKILQESHQQALDDLQAEEDKVNTLAKAKGK 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 60; DB 13; 42.4%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1931 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00612; IQ; 2, Pfam; PF00063; myosin_head; 1. Pfam; PF01576; Myosin_N; 1, Pfam; PF01576; Myosin_tail; 1. PRINTS; PR00194; TROPOMYOSIN. PRODOM; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Blochem. 246:380-387(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
InterPro; IPR000533; Tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head
InterPro; IPR004009; Myosin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyprinus carpio (Common carp).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 42.43
Matches. 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1931 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissum-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                  TISSUB-Fast muscle;
MEDLINE-97176447; PubMed-9023993;
Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
"CDNA cloning of myosin heavy chain isoforms from carp fast skeletal muscle and their gene expression associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom!;
Actinopterygil; Neopterygil; Teleostel; Buteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygil; Percomorpha; Perciformes; Percoidel;
NCBI_TaxID-118565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60; DB 13; Length 1092;
Pred. No. 94;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Fast muscle;
Yoon S., Kakinuma M., Hirayama Y., Yamamoto J., Watabe S.;
"coNn cloning and characterization of the complete primary st
myosin heavy chain from white croaker fast skeletal muscle."
Submitted (MAR-2000) to the EWBL/GenBank/DDBJ databases.
EMBL; AB039672; BAB12571.1;
HSSP; P13538; ZMYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1930;
                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 1 1 1 SEQUENCE 1092 AA; 125885 MW; B6BABBA3963BEBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221208 MW; C6219EB07CB4C5A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60; DB 13;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 KEDNVLVESHEKSLG; - EANKADVNVLTKAKSQ 51
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                                                                                                                                                                                                     acclimation.";
J. Exp. Biol. 200:27-34(1997).
EMBL; D50475; BAA09068.1;
Interpro; IPR002928; Myosin_tail.
Pfam; PF01576; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roDom; PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02736; Myosin_N; 1,
Pfam; PF01576; Myosin_tail; 1,
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 23.7%;
Best Local Similarity 42.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2002 (TrEMBLrel. 22, Myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%;
1 Similarity 42.4%;
14; Conservative
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SMART; SM00242; MYSC; 1.
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SEQUENCE 1930 AA;
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SEQUENCE FROM N.A.
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STRANDEDNESS:
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US-09-044-536A-7
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166.755 Million cell updates/sec
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                                                                                                                                                                   October 9, 2003, 08:08:57; Search time 12.9403 Seconds
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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-08-142-551B-119
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match 1
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Perfect score:
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19408, A
3, Appli
21575, A
5584, Ap
14, Appl
188, App
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APPLICANT: NARAGAWA, Shizue
APPLICANT: HABASHITA, Junko
APPLICANT: HABASHITA, Junko
APPLICANT: TARETOMI, Shigehisa
TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 Water Street
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANIC SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,536A
FILING DATE: 19-MAR-1998
APPLICATION NUMBER: 08/662,871
FILING DATE: 12-JUN-1996
ATTORNEY. AGENT INFORMATION:
NAME: COMLIN, DAVId G
REGISTRATION NUMBER: 45509-DIV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                     US-09-252-991A-21575
US-09-134-001C-5584
US-09-154-008-14
US-08-961-083-18
US-09-536-784-188
US-08-624-125-17
US-08-937-155-17
US-08-252-991A-19405
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US-09-252-991A-23620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7, Application US/09044536A
>. 6025467
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Boston
STATE: Massachusetts
COUNTRY: US
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Length 51;

Score 248; DB 3; Pred. No. 6.3e-28;

98.0%; 98.0%;

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1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KRONES, K. Anne
APPLICANT: BOZZATO, Richard P.
TITLE OF INVENTION: BONE-STIMULATING, NON-VASOACTIVE
TITLE OF INVENTION: PARATHYROID HORMONE VARINATS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863.014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                    Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: Foley & Lardner
1800 Diagonal Road, Suite 500
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APPLICATION NUMBER: US/08/332,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,680
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   FILING DATE: 19920403
CLASSIFICATION: 530
ATTORNET/AGENT INFORMATION:
NAME: BENT, Stephen A., RECISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1677
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08332453
Patent No. 5599792
GENERAL INFORMATION:
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IBM PC compatible
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llarity 98.0%;
Conservative
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                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-07-863-014-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity.
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COUNTRY: USA
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                                                                                                                                                           Sequence 3, Application US/10002818
Patent No. 6524788
GENERAL INFORMATION:
APPLICANT: Cantor, Thomas L.
TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroid Hoz
TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
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Patent No. 6524788
GENERAL INFORMATION:
APPLICANT: Cantor, Thomas L.
TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parities OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
           Gaps
                                  1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 51
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Pred. No. 6.3e-28;
1; Mismatches 0; Indels
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BOZZATO, Richard P.
RVENTION: STABILITY-ENHANCED VARIANTS OF
RVENTION: PARATHYROID HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 248; DB 4; Lu
Pred. No. 1.2e-27;
1; Mismatches 0;
     Mismatches
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/002,818
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Microsoft Word 2000 - ASCII format
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CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Microsoft Word 2000 - ASCII format
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07863014
Patent No. 5382658
GENERAL INFORMATION:
APPLICANT: KROMIS, K. Anne
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Best Local Similarity 98.0%;
Matches 50; Conservative
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Best Local Similarity 98.0%;
Matches 50; Conservative
   Conservative
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TITLE OF INVENTION: S
TITLE OF INVENTION: P
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                         FILE REFERENCE:
 50;
                                                                                                                                               US-10-002-818-3
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-002-818-3
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Matches
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Gaps

Length 84;

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Gaps

us-09-928-048a-5.rai

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1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                         34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNLTKAKSQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.0%; Score 248; DB 2; Length 84; 98.0%; Pred. No. 1.2e-27;
                                                                                                                                                                                                                                                                           APPLICANT: NISHIMURA, OSAMU
APPLICANT: KURIYAMA, MASALO
APPLICANT: KURIYAMA, MASALO
APPLICANT: KOTAMA, No. 5861284 uyuki
APPLICANT: KOTAMA, No. 5861284 uyuki
APPLICANT: KOTAMA, No. 5861284 uyuki
APPLICANT: KOTAMA, Nouneniko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
CORRESPONDENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
    Pred. No. 1.2e-27;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS SOFTWARE: FSALSEQ VETSION 1.5 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
PREPERPRIOR OF THE NUMBER: 34,235
                                                                                                                                                                                              US-08-835-231-9; Sequence 9, Application US/08835231; Patent No. 5861284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: 4161
TELECOMMUNICATION INFORMATION:
TELEFRAN: 617-523-5440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
2IP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MINITER: IBM Compatible
  Best Local Similarity 98.0%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DIKE, BRONSTE
STREET: 130 WATER STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 98.07
Best Local Similarity 98.07
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-835-231-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o
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                                                                                                                                                                            RESULT 7
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                                                                                                                                                                                                                                                                                                                                                              1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FUKUDA, TSUNCHIKO
APPLICANT: FUKUDA, TAKAO
APPLICANT: SAMADA, TAKAO
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN
TITLE OF INVENTION: PARATHYROID HORMONE
TITLE OF SEQUENCES: 18
NUMBER OF SEQUENCES: 18
ADDRESSEE: ADDRESSE:
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                    Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 84;
                                                                                                                                                                                                                                                                                                                          0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM.PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
                                                                                                                                                                                                                                                                             98.0%; Score 248; DB 1;
98.0%; Pred. No. 1.2e-27;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
REFERENCE/DOCKET NUMBER: 16777/182 ALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
REFERENCE/DOCKET NUMBER: 41,288
TELECHOUNICATION INFORMATION:
TELEFAX: (617)523-3400
TELEFAX: (617)523-6440
TELEFAX: 20021 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,197
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/016,171
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08689190 Patent No. 5714349
             TELECOMMUNICATION INFORMATION
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.08;
                                                                   TELEX: 899149
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 aming acids
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 amino acids
                                                                                                                                                                                                            ) MOLECULE TYPE: protein US-08-332-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-689-190-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 9
...thes 50; Conservat,
                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: FUKUDA.
                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FILING DATE: 19-MAR-1998
DIKE, BRONSTEIN, ROBERTS & CUSHMAN
                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/662,871
FILING DATE: 12-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN' DAVIG G
REGISTRATION NUMBER: 27,026
RECISTRATION NUMBER: 46509-D:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SISTEM: PC-DOS/MS
              130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site LOCATION: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
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                                                                                                                                                                                                                         FILING DATE: 19-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 16,17
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: MODIfied-
LOCATION: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 10
OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
                                                                                      02109
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LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION
                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAKAGAWA, Shizue
HABASHITA, Junko
TAKETOMI, Shigehisa
WENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masayuki
PROCESS FOR PRODUCTION OF SECRETORY KEX2
DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.2e-27
1; Mismatches
                                                                                                                                                                                                                                                       ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
SITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,918
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-073217
FILING DATE: 04-MAR-1996
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-352580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 8-352580 FILING DATE: 16-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/09044536A Patent No. 6025467 GENERAL INFORMATION:
                                                              Application US/08805918
                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible YSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
FELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Tsunehiko
                                                                                                                                   Poyofum1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.0%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                     SUZUKI,
YABUTA,
                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TAKETOM:
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-044-536A-36
                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-805-918-3
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OTHER INFORMATION: Xaa- acidic amino acid, basic amino acid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xaa- aliphatic neutral amino acid, basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xaa= non-charged hydrophilic amino acid-
basic amino acid;
OTHER INFORMATION: Xaa-hydrophobic alpha amino acid, basic OTHER INFORMATION: amino acid;
                                                                                                                                    OTHER INFORMATION: Xaa-Gly, Ala, Ser, Lys, Orn;
                                                                                                                                                                                                                      LOCATION: 13
OTHER INFORMATION: X8a- basic amino acid;
                                                                                                                                                                                                                                                                                                                                 LOCATION: 14
OTHER INFORMATION: Xaa basic amino acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 21
OTHER INFORMATION: Xaa- a
OTHER INFORMATION: amino
FEATURE:
NAME/KEY: Modified-site
```

NUMBER OF SEQUENCES: 3

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GENERAL INFORMATION:
APPLICANT: Cantor, Thomas L.
APPLICANT: Cantor, Thomas L.
TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyrc
TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/002,818
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE MICROSOft Word 2000 - ASCII format
SEQ ID NO 1
LENGTH: 84
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BioNebraska, inc.
VENTION: PRODUCTION OF PEPTIDES USING
VENTION: RECOMBINANT FUSION PROTEIN CONSTRICTS
                                                                                                                                                                                  Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: human parathyroid hormone peptide fragment US-10-002-818-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 248; DB 4; L
Pred. No. 1.2e-27;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Merchant & Gould
:: 3100 Norwest Center, 90 S. 7th Street
Minneapolis
                                                                                                                                                                             Score 248; DB 3;
Pred. No. 1.2e-27;
1; Mismatches :0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRIES

ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Application PC/TUS9515800 GENERAL INFORMATION: APPLICANT: BioNebraska, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,530
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10002818
Patent No. 6524788
                                                                                                                                                                           Query Match
Best Local Similarity 98.0%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.0%;
Matches 50; Conservative
                                                                                             N-terminal
                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PRO TITLE OF INVENTION: REC NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
           linear
                                            HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N- ORIGINAL SOURCE: US-09-108-661-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 31
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                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-10-002-818-1
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                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                               Xaa acidic amino acid, aliphatic neutral
amino acid;
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                        Xaa- non-charged hydrophilic amino acid,
basic amino acid;
                                                                                                                                                                                                                                                                                               Score 248; DB 3; Length 84;
Pred. No. 1.2e-27;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NISHLWIRA, Osamu
APPLICANT: NISHLWIRA, Masato
APPLICANT: KURIYAMA, Masato
APPLICANT: KURIYAMA, Masato
APPLICANT: KUYAWA, No. 6297806uyuki
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICAN
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
                 OTHER INFORMATION: Xaa- basic amino acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FOSSISCH Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 024841
FILING DATE: 18-OCT-1991
ATTORNEY AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRANDEN NUMBER: 34,235
REGISTRANDEN NUMBER: 34,235
REGISTRAND NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09108661
Patent No. 6287806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.0%;
Matches 50; Conservative
                                                                                                                                                                  NAME/KEY: . Modified-site LOCATION: 30
                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           OTHER INFORMATION: ALUS-09-044-536A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                  LOCATION: 27
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02109
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-108-661-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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Gaps

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Active Fragments and Correlated Peptides, for The Pre
Pharmaceutical Compositions Useful for The Treatment
                                                                                                                                                                                                                                                                                              1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                                                                                                                                                                                                                                                                                                                     14 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVDVLTKAKSQ 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSO 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                     /note= "84 amino acid PTH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 243; DB 2;
Pred. No. 6.1e-27;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Franco
Use of Parathormone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/EP93/02755
FILING DATE: 08-OCT-1993
APPLICATION NUMBER: NI-92A002331
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: PALMESE, MAITA LUISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect 6.1 for Winc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,726
FILING DATE: 05-ARR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08411726
Patent No. 5880093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.0%;
96.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.17
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 3
                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-411-726-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Flc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: U.
TITLE OF INVENTION: A.
TITLE OF INVENTION: P.
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Kenyon & STREET: 1 Broadway CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTIC
                                                                                                                                COCATION: 1, 84
COTHER INFORMATION:
US-08-142-5518-1
                                                                                                            NAME/KEY: Protein
                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 248; DB 5; Length 84
Pred. No. 1.2e-27;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993.
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08142551B
Patent No. 5814603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000
NAME: Carter, Charles G
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.0%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      699 Prince Street
                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                  internal
                                                                                                    TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alexandria
                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                               잋
                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-15800-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-142-551B-1
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Score 238; DB 1; Length 84;
Pred. No. 3.1e-26;
3; Mismatches 0; Indels
                                    Sequence 1, Application US/07707114
Patent No. 5208041
GENERAL INFORMATION:
APPLICANT: SINDREY, Dennis R.
TITLE OF INVENTION: ESSENTIALLY PURE HUMAN PARATHYROLD TITLE OF INVENTION: HORMONE NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Folly & Lardner STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/707,114
FILING DATE: 19910523
CLASSIFICATION: 424
ATONNEY/AGENT INPORMATION:
NAME: BENTY: Stephen A
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEPHONE: (703) 836-9300
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELERAK: (703)683-4109
TELERX: 893149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 84 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapiens
IMMEDIATE SOURCE:
CLONE: hPTH
US-07-707-114-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.1%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                  STATE: VA
RESULT 15
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Gaps

Search completed: October 9, 2003, 08:15:10 Job time : 12.9403 secs

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Thu Oct 9 09:35:54 2003
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

/pubpaa/US10B_PUBCOMB.pep:* /pubpaa/US10C_PUBCOMB.pep:* /pubpaa/US10_NEW_PUB.pep:*

ptodata/1/

NEW PUB.

pubpaa/US10A_PUBCOMB

pubpaa/US09B_PUBCOMB.pep: 'pubpaa/US09C_PUBCOMB.pep: 'pubpaa/US09_NEW_PUB.pep:*

pubpaa/US09A_PUBCOMB.pep

Pubpaa/PCTUS_PUBCOMB.

/pubpaa/PCT_NEW_PUB

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Description	:		00			ì	•	ın	m	,	Sequence 12. Appl	Sequence 1. Appl	Segmence 10. Anni	Sequence 1 Appli	Sequence 50, Appl
QI.	US-09-928-047B-3	US-09-928-048A-5	US-09-928-047B-8	US-09-928-047B-4	US-09-928-047B-2	US-09-928-047B-1	US-09-928-048A-4	US-09-928-047B-5	US-09-928-048A-3	US-10-215-770-1	US-09-843-221A-12	US-09-169-786-1	US-09-843-221A-10	US-09-898-398-1	US-10-157-031-50
DB	97	12	10	10	10	10	12	10	12	15	Ħ	6	Ξ	11	15
Length	51	21	57	78	82	83	83	84	8	84	78	84	84	84	115
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.0	98.0	98.0	98.0	98.0
Score	253	253	253	253	253	253	253	253	253	253	248	248	248	248	248
Result No.	н	8	m	₹7	'n	ø	7	ത	ch	10	11	12	13	14	15
	Query Score Match Length DB ID	% Query Score Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 Sequence 3	Ouery Score Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 51 12 US-09-928-048A-5 Sequence 5	Query Score Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 51 10 US-09-928-048A-5 Sequence 5, 253 100.0 57 10 US-09-928-047B-8 Sequence 6, 259 100.0 57 10 US-09-928-047B-8	Query Score Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 51 10 US-09-928-048h-5 Sequence 5, 253 100.0 57 10 US-09-928-047B-8 Sequence 6, 253 100.0 78 10 US-09-928-047B-4 Sequence 6,	Score Match Length DB ID Description 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 57 10 US-09-928-047B-8 Sequence 6, 253 100.0 57 10 US-09-928-047B-8 Sequence 6, 253 100.0 78 10 US-09-928-047B-4 Sequence 6, 253 100.0 82 10 US-09-928-047B-4 Sequence 7, 253 100.0 82 10 US-09-928-047B-4 Sequence 7, 253 100.0 82 10 US-09-928-047B-2 Sequence 7, 253 100.0 82 10 US-09-928-047B-2	Score Match Length DB ID Description 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 57 10 US-09-928-047B-4 Sequence 6, 253 100.0 78 10 US-09-928-047B-4 Sequence 4, 253 100.0 82 10 US-09-928-047B-4 Sequence 4, 253 100.0 82 10 US-09-928-047B-2 Sequence 2, 253 100.0 82 10 US-09-928-047B-2 Sequence 2, 253 100.0 83 10 US-09-928-047B-2 Sequence 2, 253 100.0 83 10 US-09-928-047B-1 Sequence 1, 254 US-047B-3 Sequence 1, 254 US-047B-3 Sequence 2, 253 100.0 83 10 US-09-928-047B-3 Sequence 1, 254 US-047B-3 Sequence 1, 255 US-047B-3 Sequence 2, 255 US-047B-3 Sequence 1, 255 US-047B-3 Sequence 1, 255 US-047B-3 Sequence 2, 255 US-047B-3 Sequence 2, 255 US-047B-3 Sequence 3, 255 US-047B-3	Score Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 51 10 US-09-928-047B-8 Sequence 5, 253 100.0 78 10 US-09-928-047B-8 Sequence 6, 253 100.0 78 10 US-09-928-047B-8 Sequence 4, 253 100.0 82 10 US-09-928-047B-2 Sequence 2, 253 100.0 83 10 US-09-928-047B-1 Sequence 2, 253 100.0 83 10 US-09-928-047B-1 Sequence 1, 253 100.0 83 10 US-09-928-047B-1 Sequence 1, 253 100.0 83 10 US-09-928-047B-1 Sequence 1, 253 100.0 83 10 US-09-928-047B-1	Score Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 57 10 US-09-928-048h-5 Sequence 6, 253 100.0 57 10 US-09-928-048h-5 Sequence 6, 253 100.0 78 10 US-09-928-047B-4 Sequence 6, 253 100.0 83 10 US-09-928-047B-1 Sequence 1, 253 100.0 83 12 US-09-928-047B-1 Sequence 1, 253 100.0 83 12 US-09-928-047B-1 Sequence 1, 253 100.0 84 10 US-09-928-047B-4 Sequence 5, 253 100.0 84 10 US-09-928-047B-4 Sequence 5, 253 100.0 84 10 US-09-928-047B-5 Sequence 5, 253 100.0 84 10 US-09-928-047B-5	Score Match Length DB ID Description 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 57 10 US-09-928-047B-4 Sequence 5, 253 100.0 78 10 US-09-928-047B-4 Sequence 4, 253 100.0 82 10 US-09-928-047B-4 Sequence 4, 253 100.0 83 12 US-09-928-047B-1 Sequence 1, 253 100.0 83 12 US-09-928-047B-1 Sequence 4, 253 100.0 84 10 US-09-928-047B-1 Sequence 5, 253 100.0 84 10 US-09-928-047B-5 Sequence 5, 253 100.0 84 10 US-09-928-048A-3 Sequence 5, 253 US-09-928-048A-3 Sequence 6, 253 US-09-928-048A-	Acore Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 Sequence 3, 253 100.0 57 10 US-09-928-047B-4 Sequence 4, 253 100.0 78 10 US-09-928-047B-4 Sequence 4, 253 100.0 82 10 US-09-928-047B-2 Sequence 4, 253 100.0 83 10 US-09-928-047B-1 Sequence 1, 253 100.0 83 12 US-09-928-047B-1 Sequence 1, 253 100.0 84 10 US-09-928-047B-1 Sequence 2, 253 100.0 84 10 US-09-928-048B-5 Sequence 5, 253 100.0 84 11 US-09-928-048B-3 Sequence 5, 253 100.0 84 11 US-09-928-048B-3 Sequence 3, 253 100.0 84 115 US-09-928-048B-3 Sequence 3, 253 10	Score Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 253 100.0 57 10 US-09-928-047B-8 253 100.0 78 10 US-09-928-047B-8 253 100.0 82 10 US-09-928-047B-2 253 100.0 82 10 US-09-928-047B-2 253 100.0 83 12 US-09-928-047B-1 253 100.0 84 12 US-09-928-048A-3 258 100.0 84 12 US-09-928-048A-3 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US-09-928-047B-3 253 100.0 57 10 US-09-928-047B-8 253 100.0 87 10 US-09-928-047B-8 253 100.0 82 10 US-09-928-047B-1 253 100.0 83 10 US-09-928-047B-1 253 100.0 83 10 US-09-928-047B-1 253 100.0 84 10 US-09-928-048B-5 253 100.0 84 15 US-09-928-048B-5 253 100.0 84 15 US-09-928-048B-5 254 100.0 84 15 US-09-928-048B-5 258 100.0 84 15 US-09-943-221A-12 248 98.0 78 11 US-09-843-221A-10	Score Match Length DB ID 253 100.0 51 10 US-09-928-047B-3 253 100.0 57 10 US-09-928-047B-8 253 100.0 78 10 US-09-928-047B-8 253 100.0 82 10 US-09-928-047B-4 253 100.0 83 10 US-09-928-047B-1 253 100.0 84 10 US-09-928-047B-1 253 100.0 84 10 US-09-928-048A-4 253 100.0 84 10 US-09-928-048A-3 253 100.0 84 10 US-09-928-047B-5 253 100.0 84 10 US-09-928-048A-3 254 100.0 84 11 US-09-928-047B-1 248 98.0 78 11 US-09-843-221A-12 248 98.0 84 11 US-09-843-321A-1

7, App 4, App 4, App 2, App 2, App 11,	Sequence 3260, Ap Sequence 8260, Ap
9928 - 047 9928 -	US-10-128-714-3260 US-10-128-714-8260
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000000000000000000000000000000000000000	51.5
11111222222222222222222222222222222222	4 4 5

ALIGNMENTS

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Gaps
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TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
FILE REFERENCE: 53221-20002.00
CURRENT TILING DATE: 2001-08-10
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/224,446
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 51
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APPLICANT: Cantor, Thomas L.
TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
                     Sequence 3, Application US/09928047B Patent No. US20020160945A1 GENERAL INFORMATION:
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-09-928-047B-3
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Gaps

Indels

Pred. No. 1.3e-25; Mismatches 0;

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28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 78
                Similarity 100.0%; Pi 51; Conservative 0;
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                Best Local
Matches 5
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TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE FILE REFERENCE: 53221-20015.00 CURRENT APPLICATION NUMBER: US/09/928,048A CURRENT FILING DATE: 2000-08-10 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5 LENGTH: 51
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TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
FILE REFERENCE: 53221-20002.00
CURRENT APPLICATION NUMBER: US/09/928,047B
PRIOR APPLICATION NUMBER: US 60/224,446
PRIOR PRILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTEED for Windows Version 4.0
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TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
FILE REFERENCE: 53221-20002.00
CURRENT APPLICATION NUMBER: US/09/928,047B
PRIOR APPLICATION NUMBER: US 60/224,446
PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                          Length 51;
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Pred. No. 7.8e-26;
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Pred. No. 8.9e-26;
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Best Local Similarity 100.0%; Pred. No. 7
Matches 51; Conservative 0; Mismatche
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 78
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Best Local Similarity 100.0%;
Matches 51; Conservative 0
                                                                                                                                                                                                               ORGANISM: Homo sapiens
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US-09-928-047B-8
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US-09-928-0478-4
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                                                                                                                                                                                            TYPE: PRT
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100.0%; Score 253;

Query Match

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Gaps
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TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTRONIST OR MODULATORS AND OSTEOPOROSIS
FILE REFERENCE: 5321-20002.00
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/224,446
PRIOR RILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 82
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TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
FILE REFERENCE: 5321-20002.00
CURRENT APPLICATION NUMBER: US/09/928,047B
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/224,446
PRIOR FILING DATE: 2000-08-10
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100.0%; Score 253;
Best Local Similarity 100.0%; Pred. No. 1
Matches 51; Conservative 0; Mismatche
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Sequence 2, Application US/09928047B Patent No. US20020160945A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09928047B
Patent No. US20020160945Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-928-047B-2
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US-09-928-047B-1
                                                       GENERAL INFORMATION:
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us-09-928-048a-5.rapb

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Query Match
Best Local
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                  APPLICANT: Cantor, Thomas L.
TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
FILE REFERENCE: 53221-20015.00
CURRENT APPLICATION NUMBER: US/09/928,048A
CURRENT APPLICATION NUMBER: US/09/928,048A
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
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TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
FILE REFERENCE: 53221-20015.00
CURRENT APPLICATION NUMBER: US/09/928,048A
CURRENT FILING DATE: 2000-08-10
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TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
FILE REFERENCE: 53221-20002.00
CURRENT APPLICATION NUMBER: US/09/928,047B
CURRENT FILING DATE: 2001-08-10
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0; Mismatches
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Scantibodies Laboratory, Inc.
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PUBLICATION NO. US20030138858A1
GENERAL INFORMATION:
APPLICANT: Scantibodies Laboratory, Inc.
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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 51; Conservative 0
                                                                                                                                                                                                                                        ) TYPE: PRT
) ORGANISM: Homo sapiens
US-09-928-048A-4
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Matches 51; Conserv
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APPLICANT: LIU, CHUAN-FA
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHY
TITLE OF INVENTION: RELATED PROTEIN
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Publication No. US20030087822A1

GENERAL INFORMATION:

APPLICATOR. CANTOR. Thomas L.

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/10/215,770

CURRENT FILING DATE: 2002-12-16

PRIOR FILING DATE: 2000-12-16

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 84
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Score 253; DB 12;
Pred. No. 1.4e-25;
Mismatches 0;
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Pred. No. 5.8e-25;
1; Mismatches 0;
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98.0%;
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                   Similarity 100.
51; Conservative
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Best Local Similarity 100.
Matches 51; Conservative
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NUMBER OF
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us-09-928-048a-5.rapb

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APPLICANT: Krukovskaya, L. L. T. TITLE OF INVENTION: In silico screening for phenotype-associated expressed scrite Reference: 2760-103
                     GENERAL INFORMATION:
APPLICANT: Hutchison, James Scott
TILLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
FILE REFERENCE: A1713
CURRENT APPLICATION NUMBER: US/09/898,398
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
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Pred. No. 9.3e-25;
1; Mismatches 0;
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98.0%;
          Publication No. US20030082179A1
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Kozlov, A. P.
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Krukovskaya, L.
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; ORGANISM: Homo saplens
US-09-898-398-1
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US-10-157-031-50
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Best Local Similarity
Matches 50; Conserv
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LENGTH: 84
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APPLICANT: LACEY, DAVID LEB
ATTILEANT: LACEY, DAVID LEB
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: RELATED PROTEIN
FILE REPRESENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
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                     28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78
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                                                                                                                                      Sequence 1, Application US/09169786B
Patent No. US20020025929A1
GENERAL INFORMATION:
APPLICANT: Sato, Masahiko
TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
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Pred. No. 6.4e-25; 1; Mismatches 0;
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Pred. No. 6.4e-25;
                                                                                                                                                                                                                                      FILE REFERENCE: X-11480
CURRENT APPLICATION NUMBER: US/09/169,786B
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,800
EARLIER FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 84
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PRIOR APPLICATION NUMBER: 60/214,860
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/200,053
PRIOR FILING DATE: 2000-04-27
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SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 84
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Best Local Similarity 98.0%;
Matches 50; Conservative
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Best Local Similarity 98.0%;
Matches 50; Conservative
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; ORGANISM: Homo saplens
US-09-169-786-1
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ORGANISM: Homo sapiens
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US-09-898-398-1
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